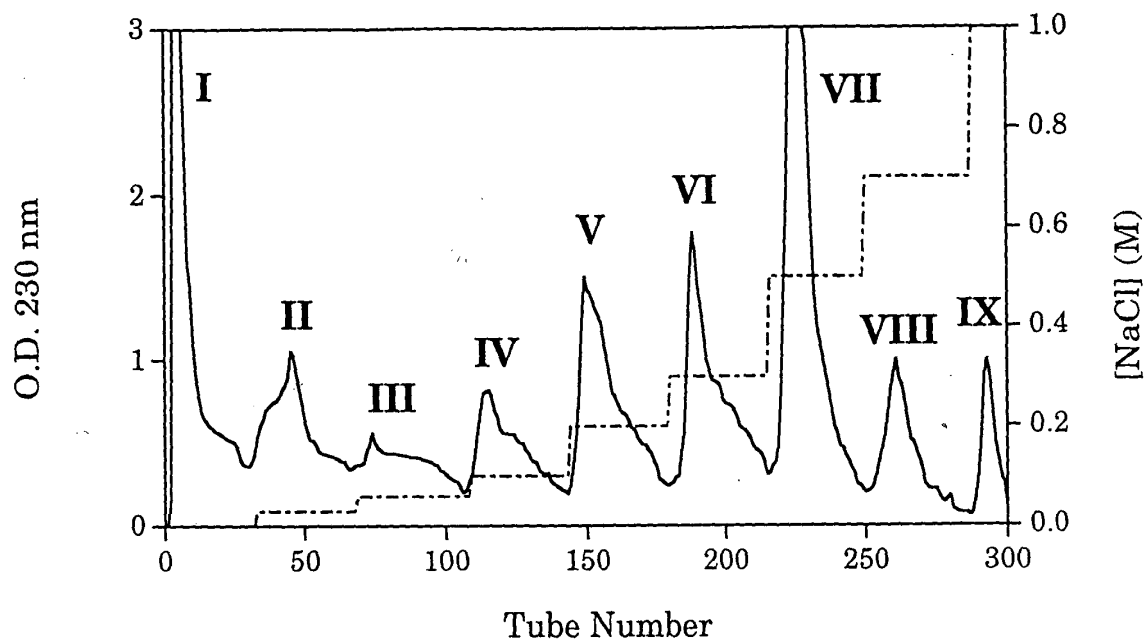


FIG 1.0

A.



B.

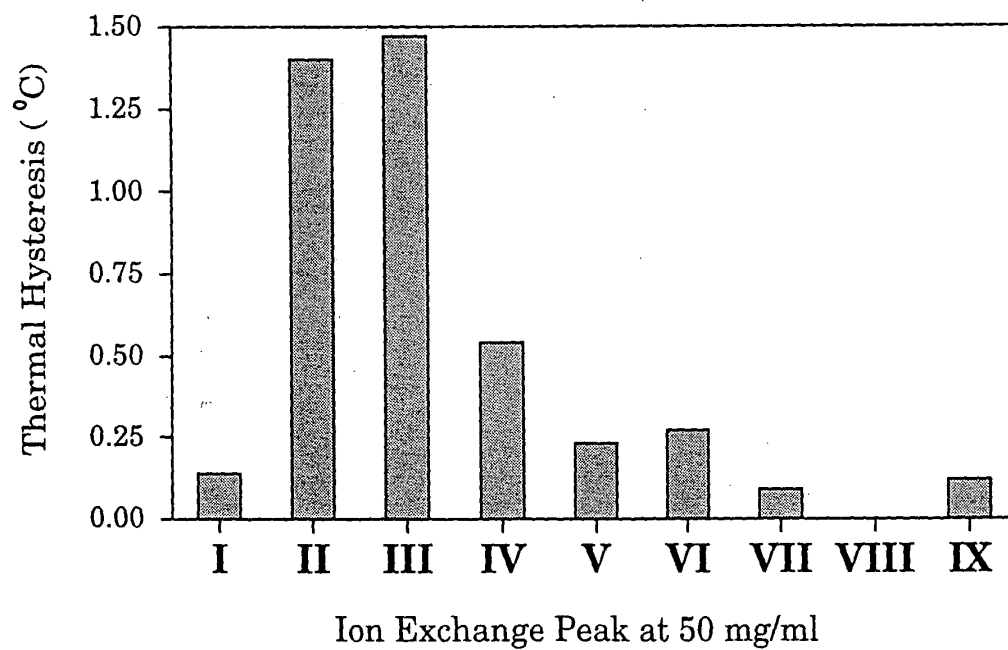


FIG 1.1

FO4090" SHE94860

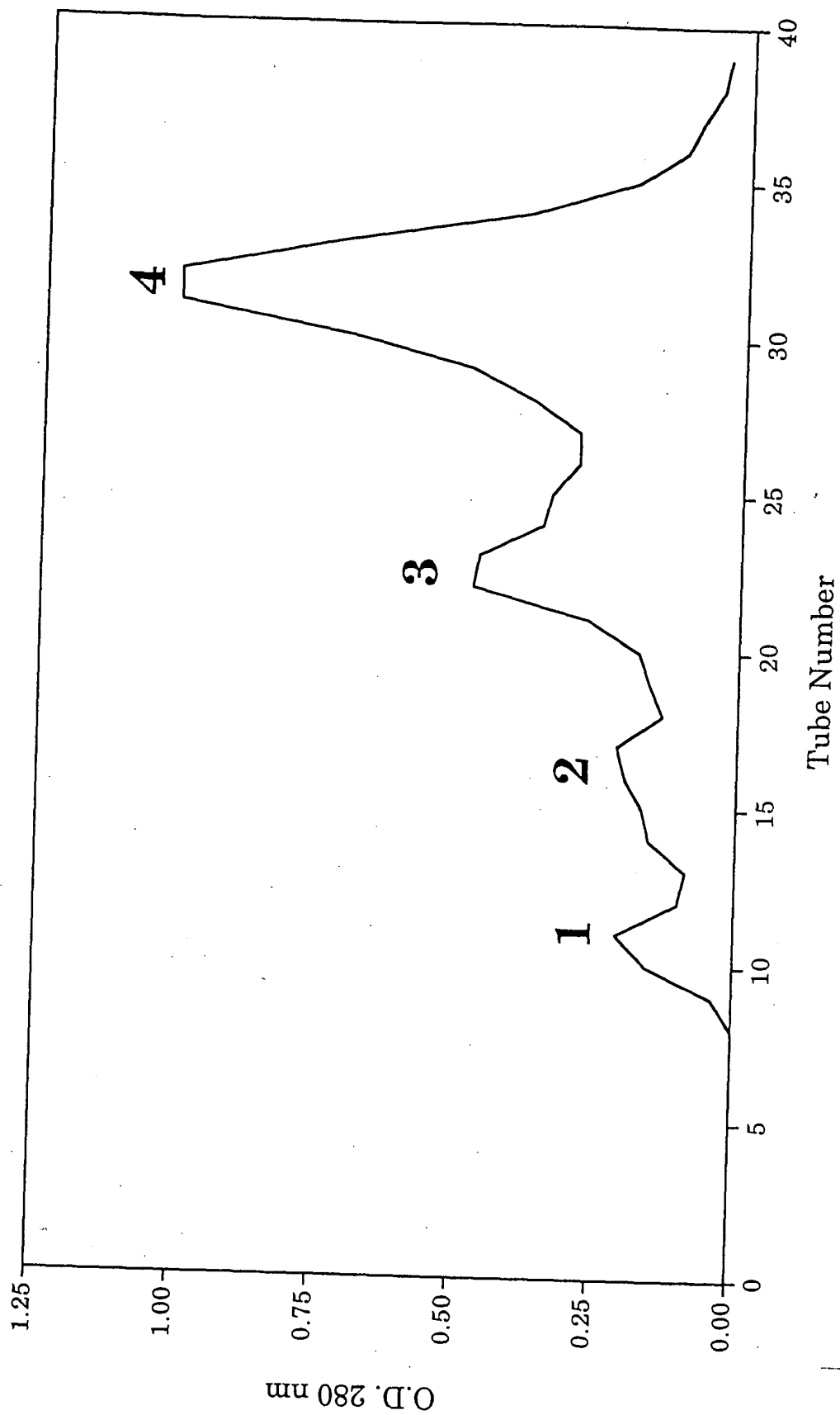


FIG 1.2

FD-2090-24E92850

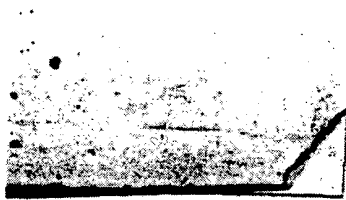


FIG 1.3

Tm-12.86

12.5 25

FIG 1.4

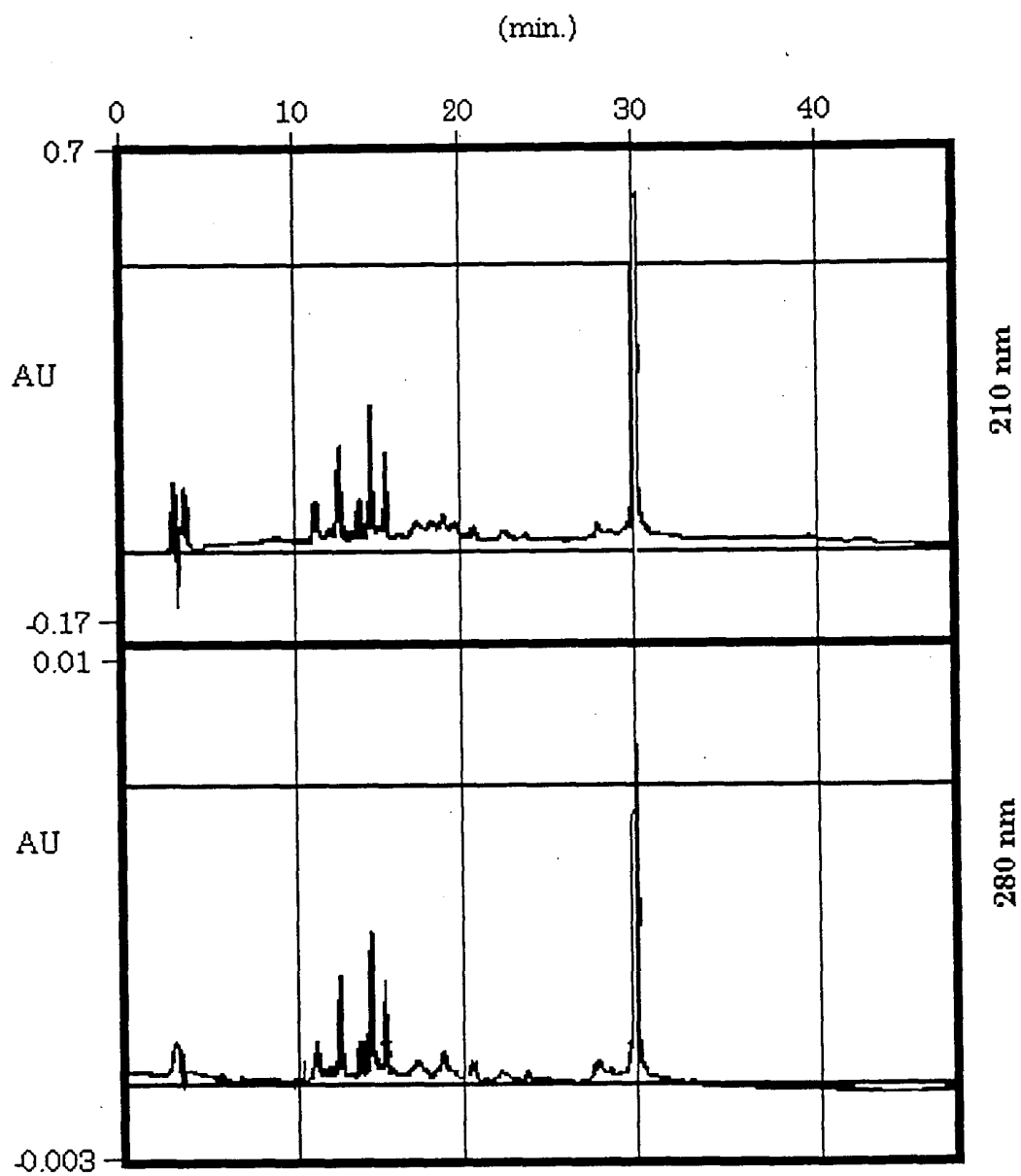


FIG 1.5

102090" 04E92860

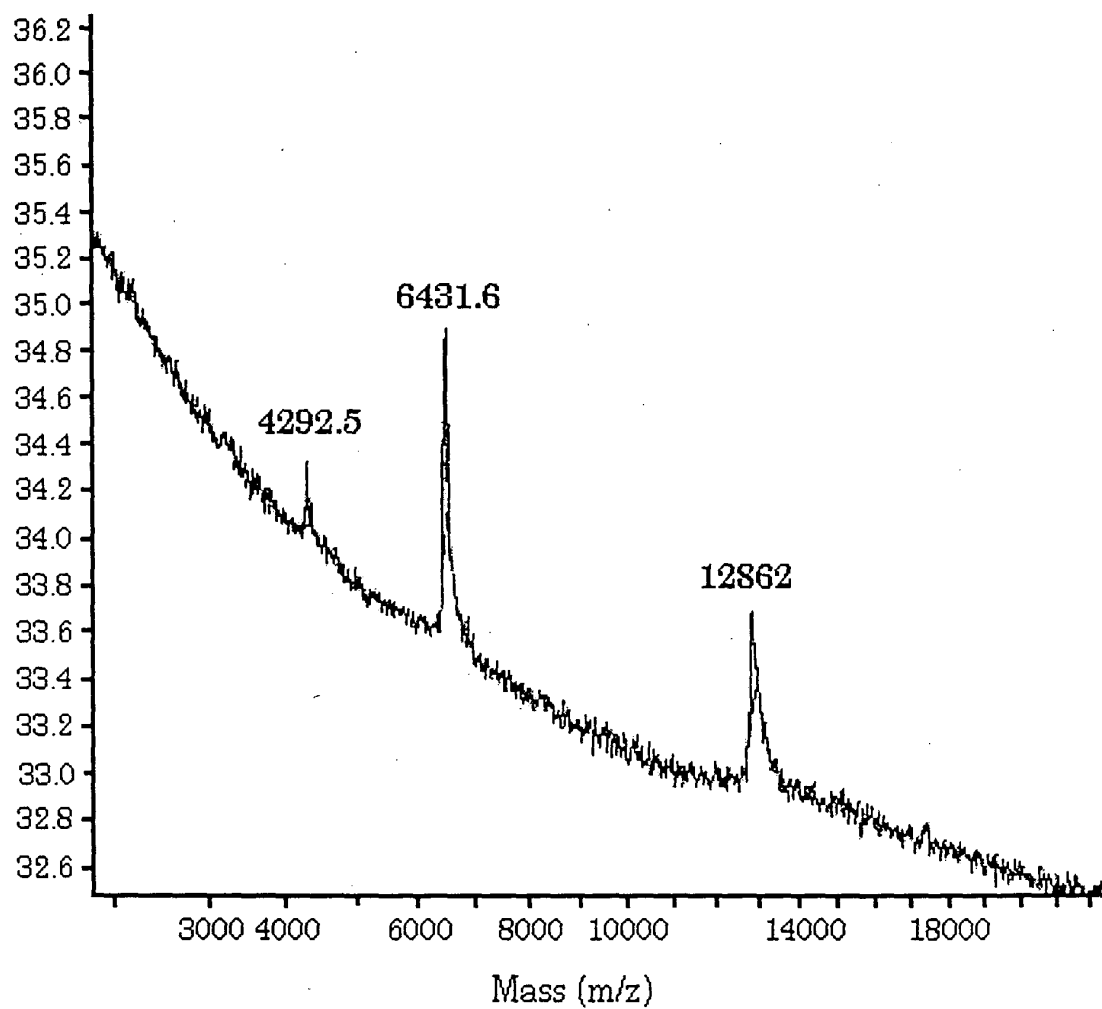


FIG 1.6

09876345-060701

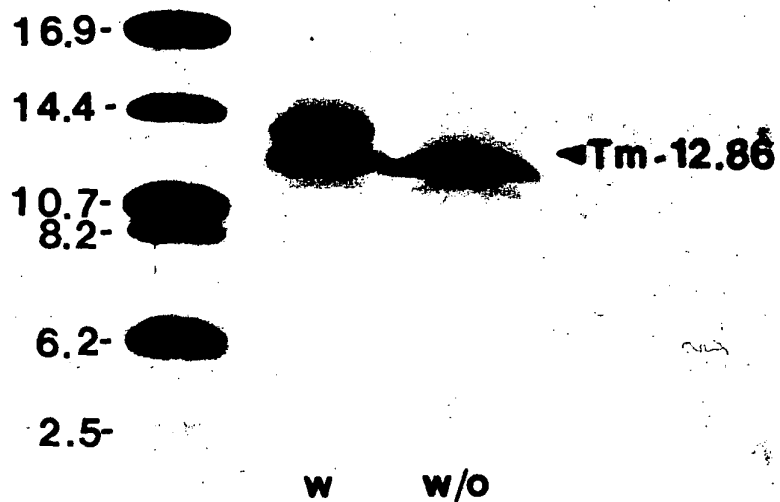


FIG 1.7

NH₂-L-T-D-E-Q-I-Q-K-R-N-K-I-S-K-E-?-Q-Q-V

Val
Gln
Gln
Glu
Lys
Ser
Ile
Lys
Asn
Arg
Lys
Gln
Ile
Gln
Glu
Asp
Thr
Leu

FIG. 1.8

09876348 . 060701

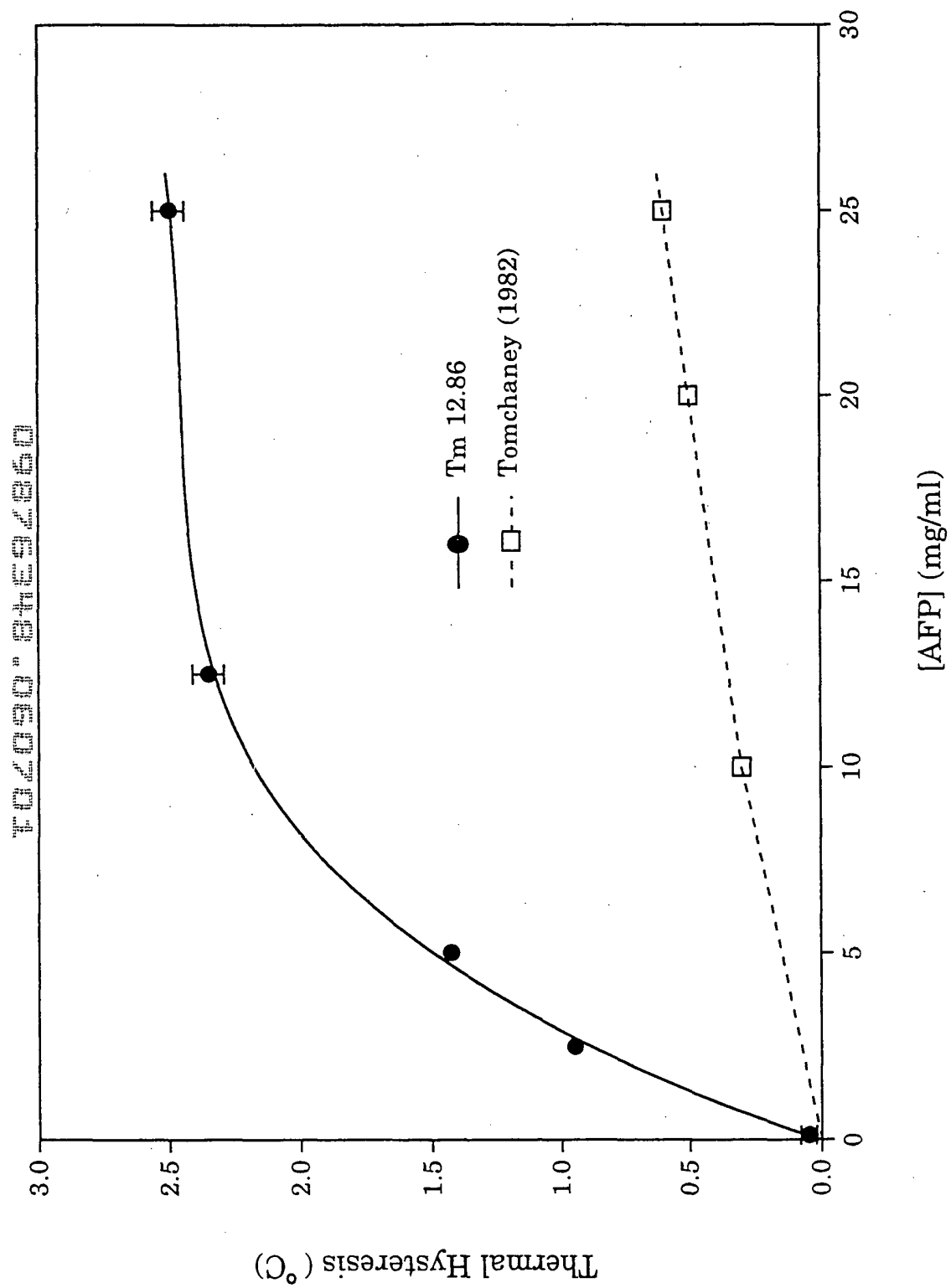


FIG 1.9

09876348-060701

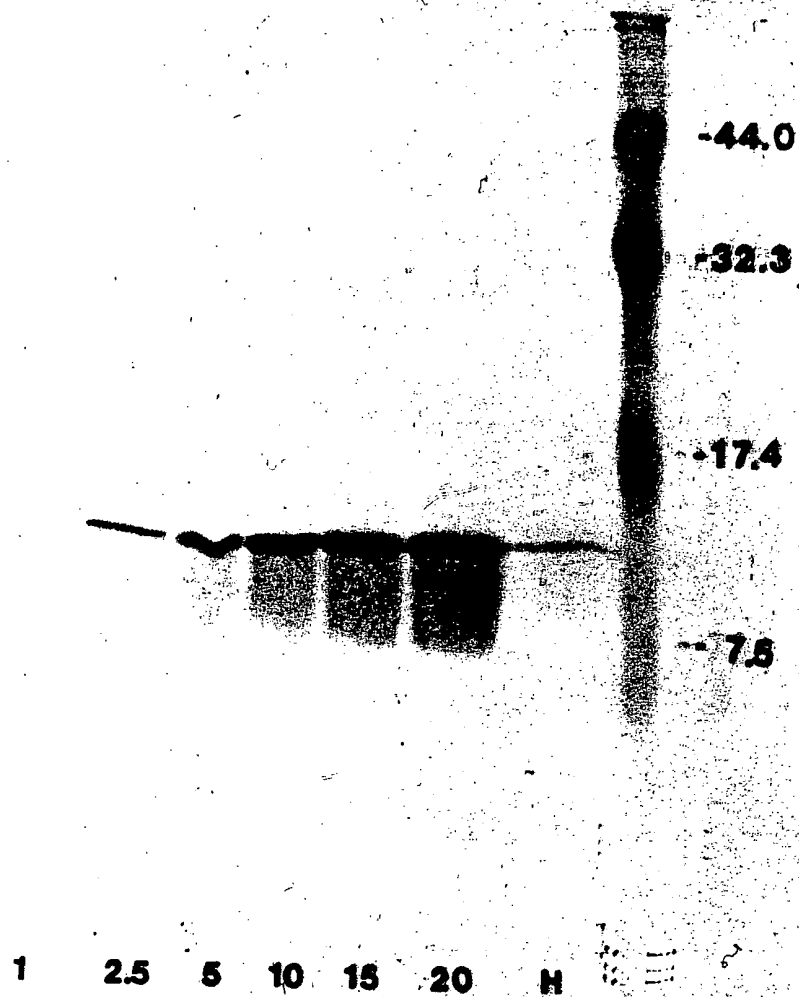


FIG 1.10

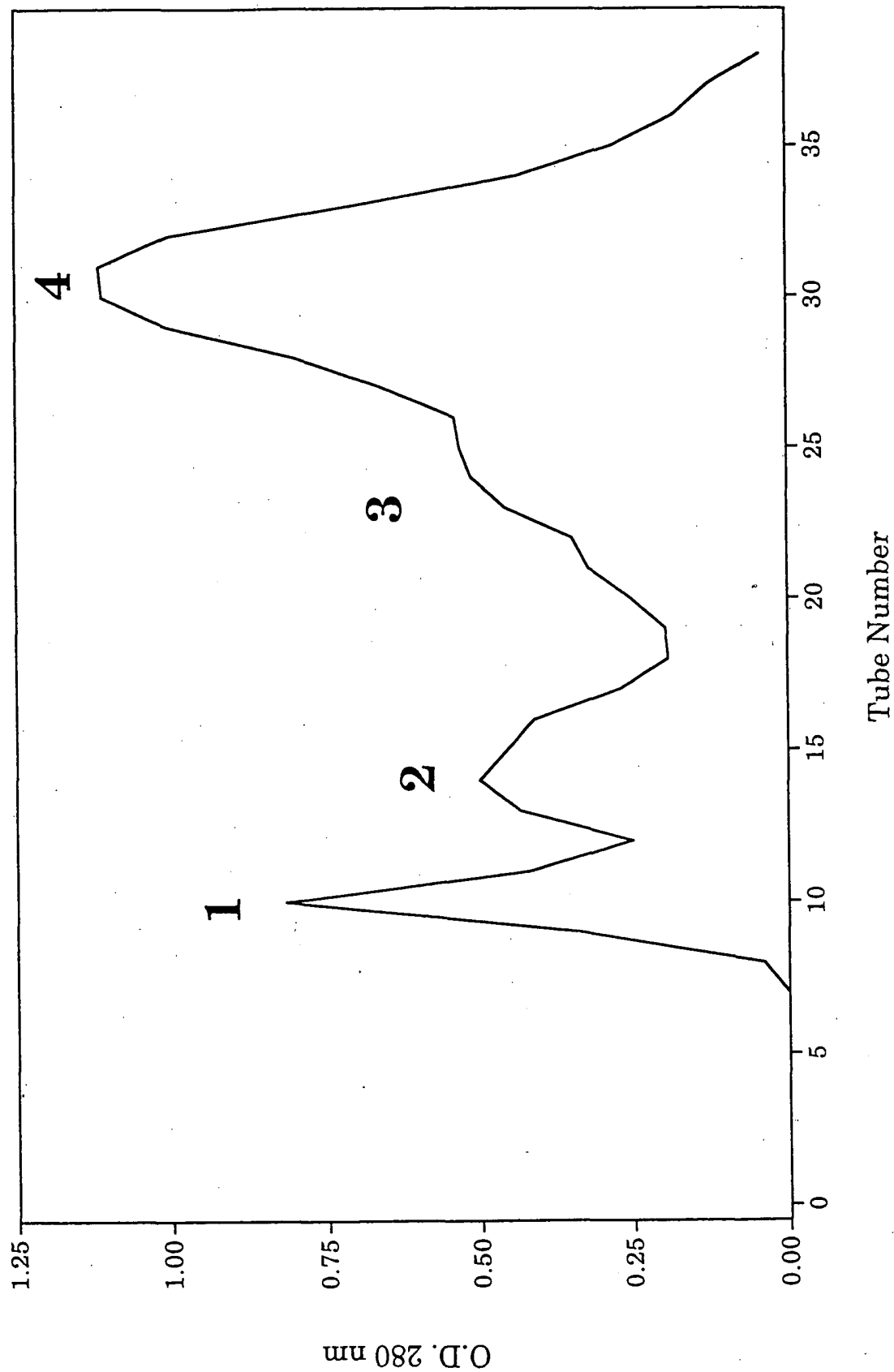


FIG 1.11

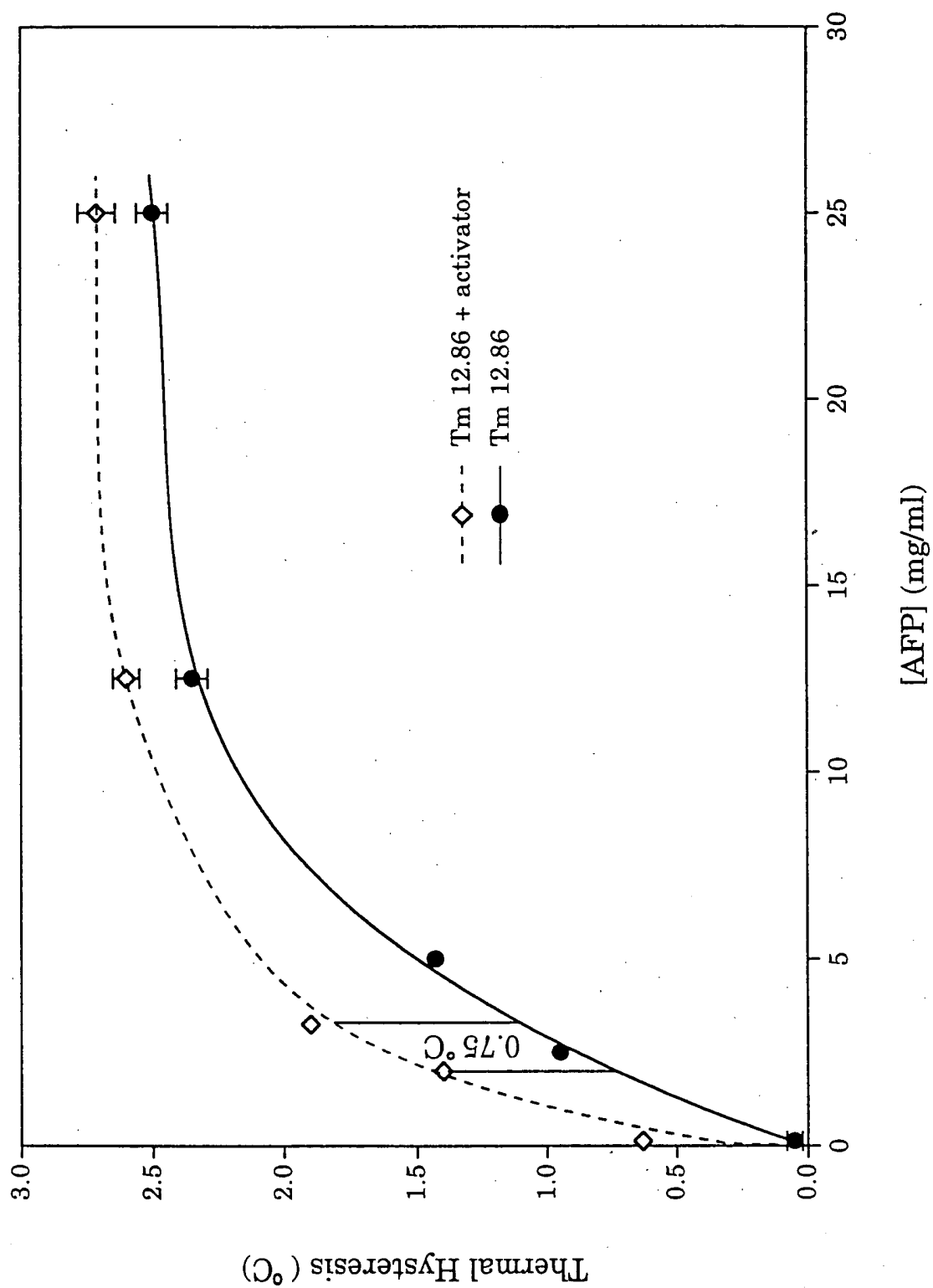


FIG 1.12

0987540-060701

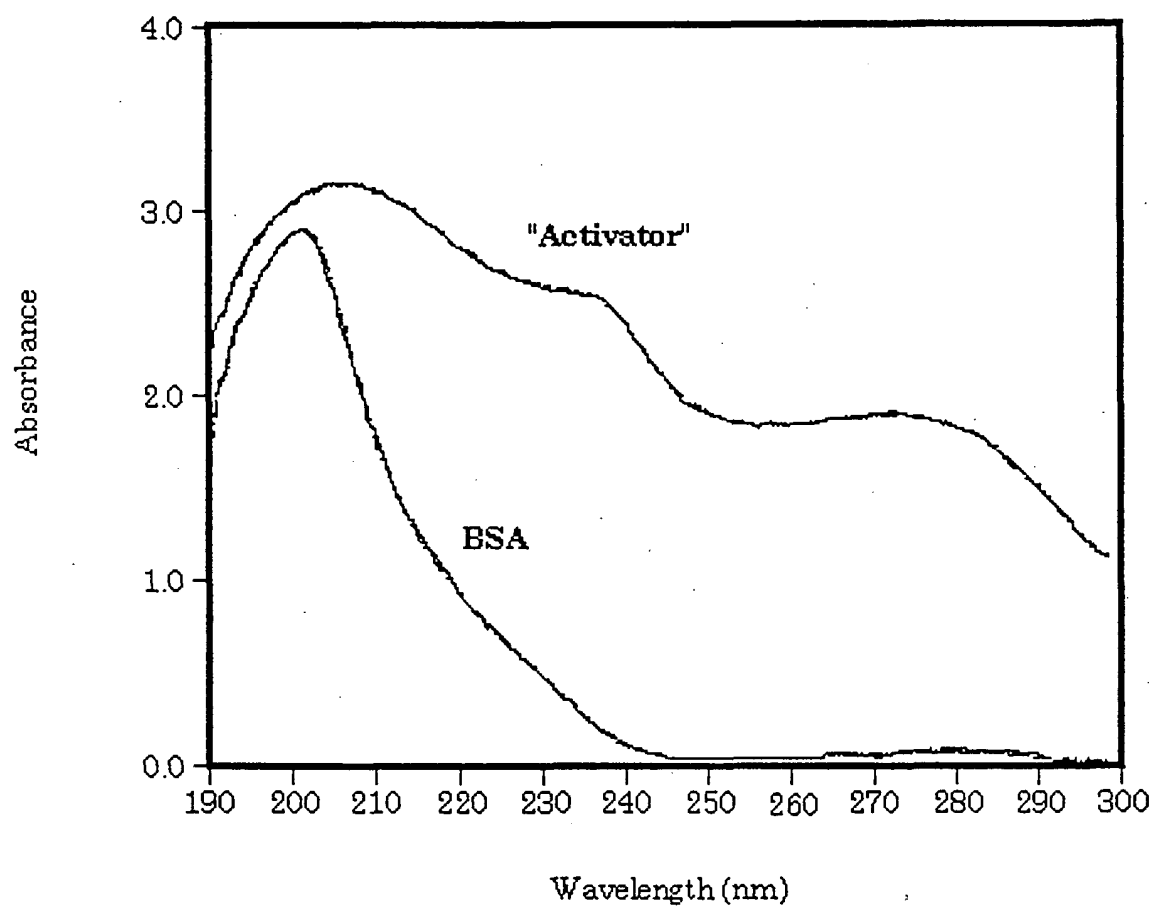


FIG 1.13

09876348-060701

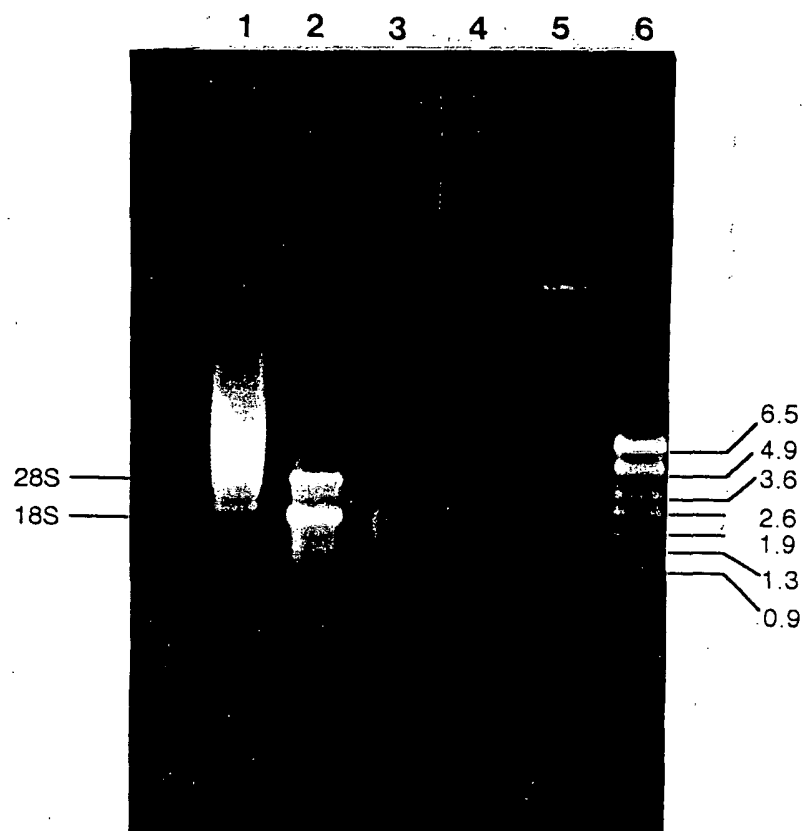


FIG 2.0

09876348-060701
T02090-87E92860

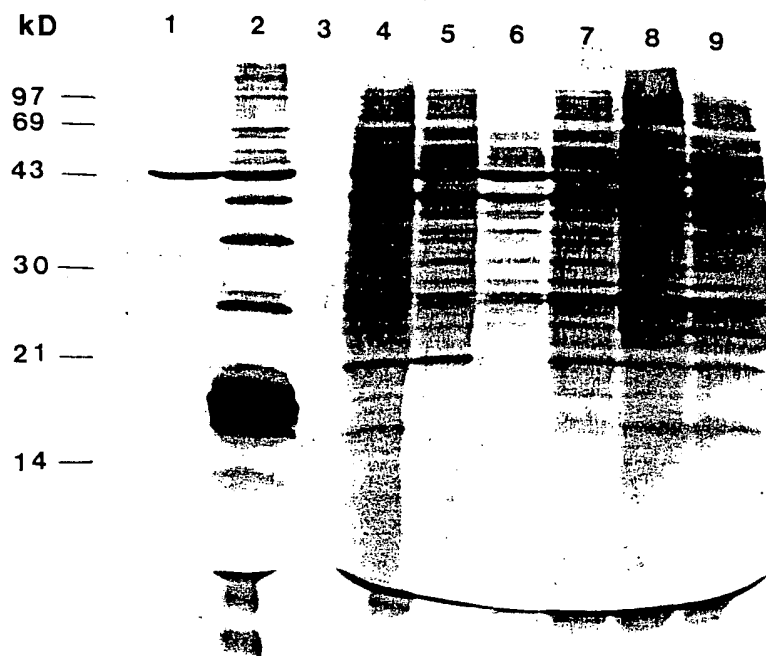


FIG 2.1

09876348-060701

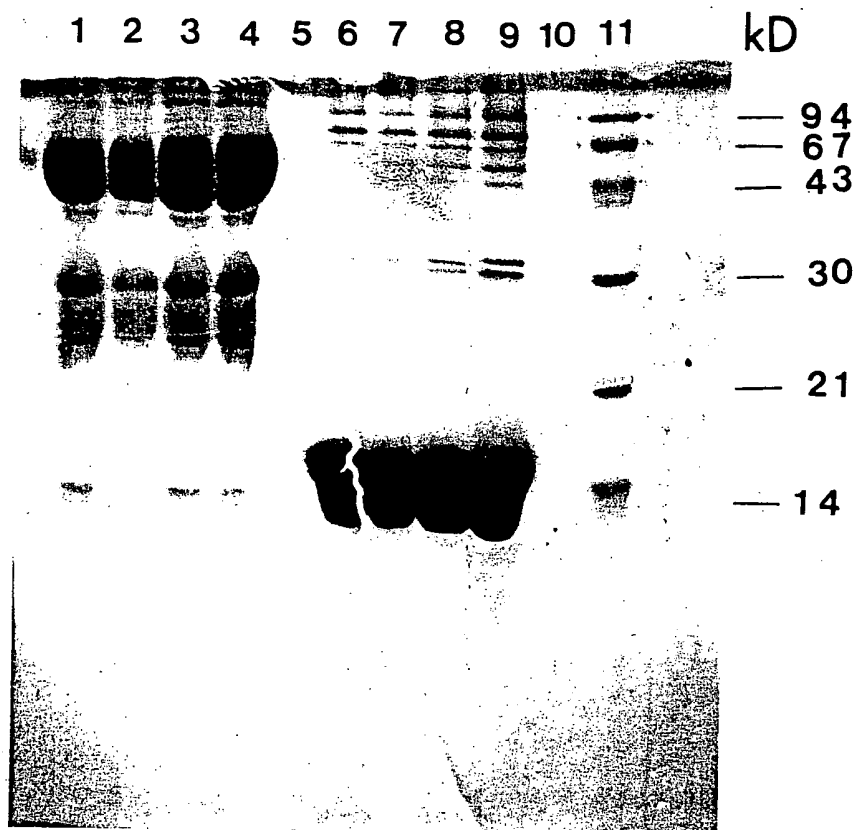


FIG 2.2

09876348 060701

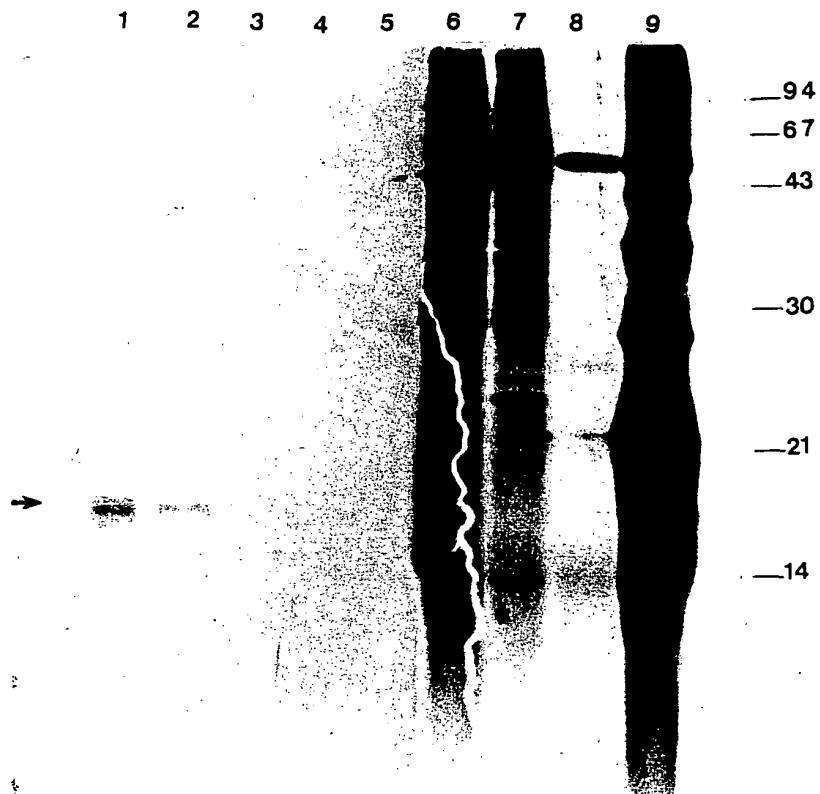


FIG 2.3

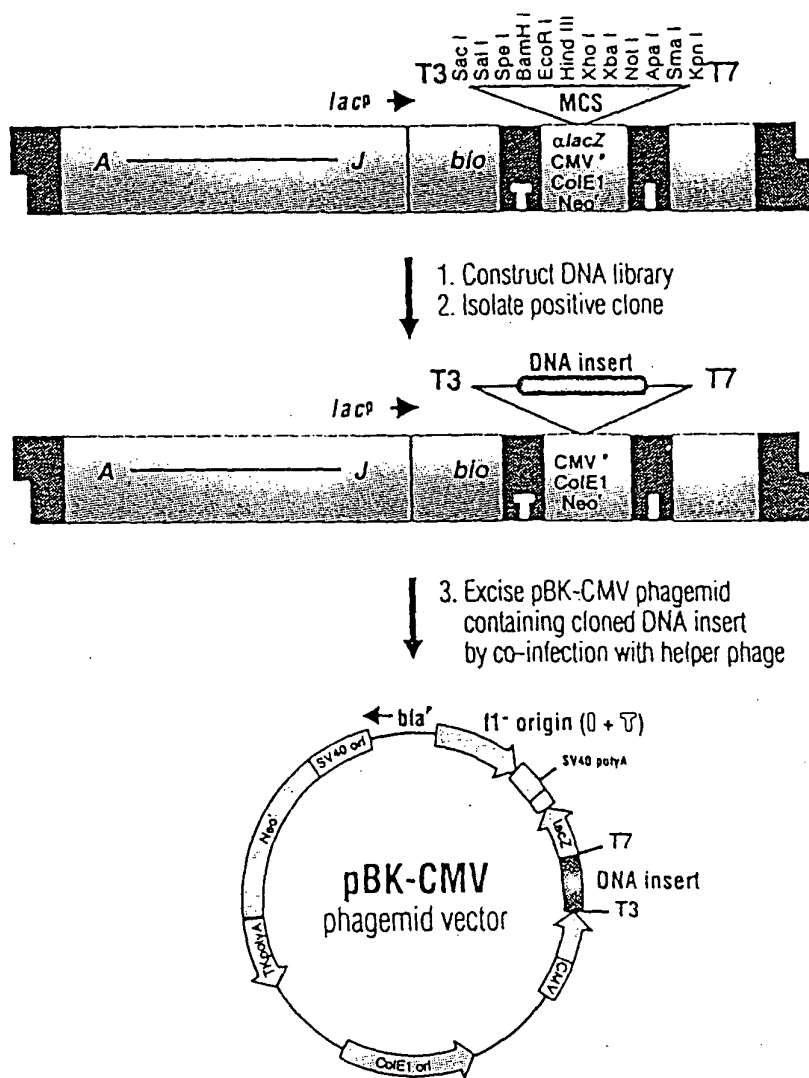


FIG. 2.4 a

09876348-060704

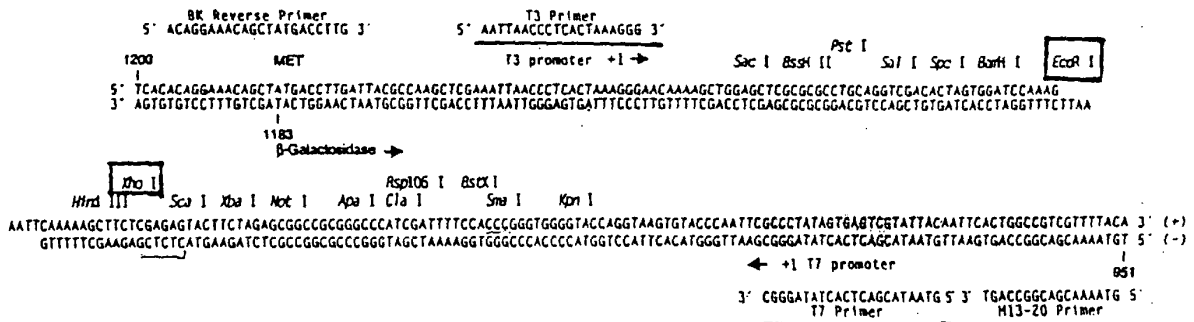
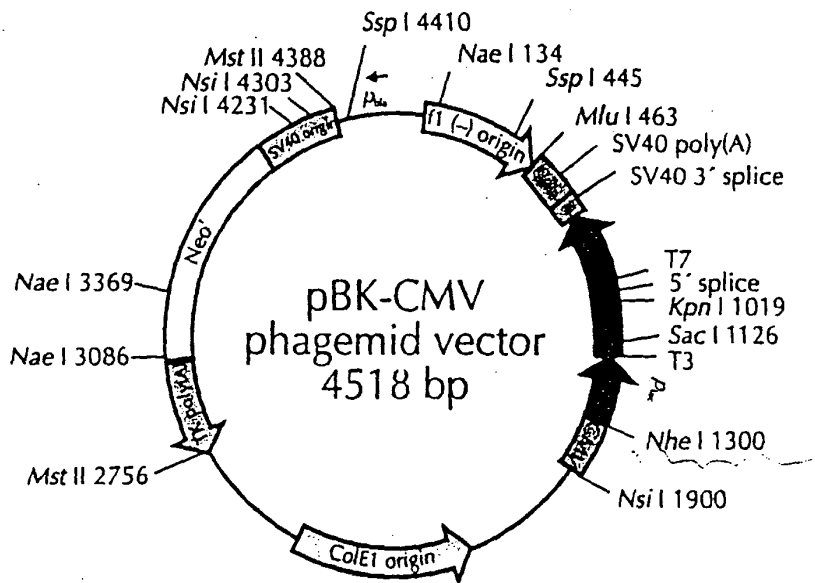


FIG. 2.4 b

09876348-060701

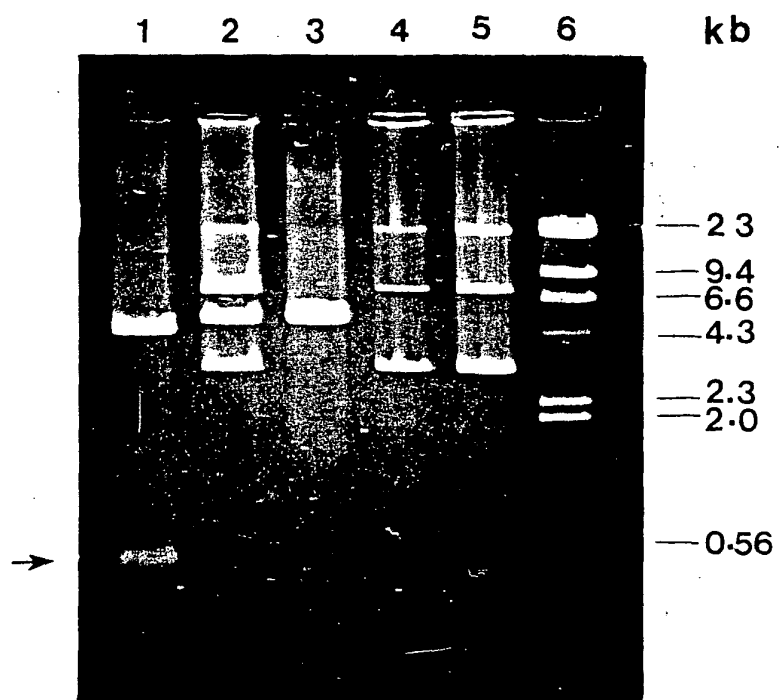


FIG 2.5

DNA sequence of Tm 13.17 cDNA clone

B	E
a	C
m	O
H	R
I	I

1 AGTGGATCCAAAGAATTTCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAACTGAAACGCCAAGTTTTTTCGTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACCTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

X
h
o
I

481 ATATAAAAAATAAAGTGTCTTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTTCCACCC

FIG 2.6a

09876348-060701

09876348.060701
T02090-87E92860

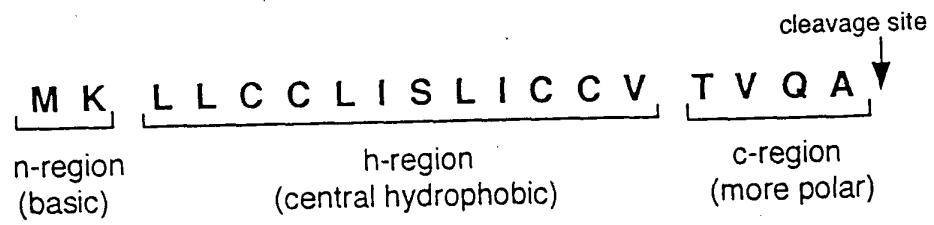


FIG 2.6b

0976316-0601

0976316-0601

[illegible]

0976316-0624

0976316-0624

[illegible]

0976316-062

09876348.060701

Tm 13.17

AFP-3

B Protein

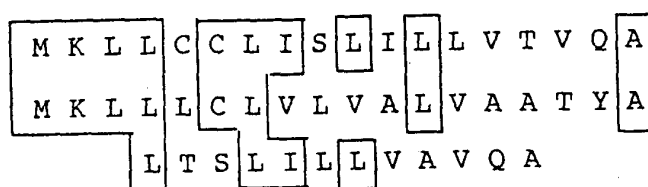


FIG 2.9

09876348-060704
102090-84E9/850

Tm 13.17	NH2	L	T	E	A	Q	I	E	K	L	N	K	I	S	K	K	C	Q	N	E
				:	:			:												
Tm 12.86	NH2	L	T	D	E	Q	I	Q	K	R	N	K	I	S	K	E	?	Q	Q	V

FIG 2.10

0587343 060701

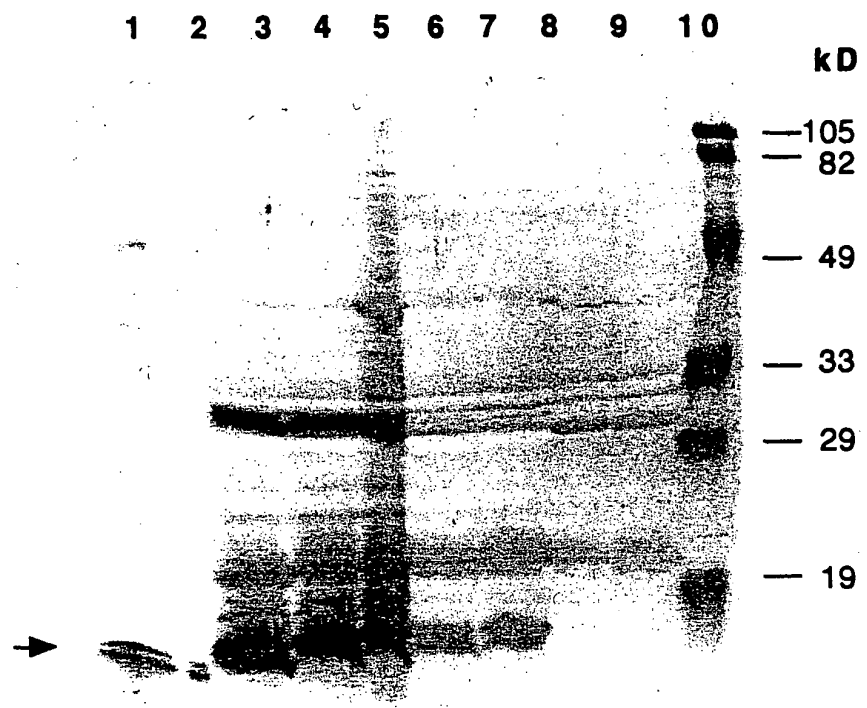


FIG 2.11

Tm 12.86 L T D E Q I Q K R N K I S K E ? Q Q V
 Tm 13.17 1 L T E A Q I E K L N K I S K K C Q N E S G V S Q E I I T K A 30
 B1 13 I T E E D L E L L R Q T S A E C K T E S G V S E D V I K R A 43
 AFP-3 1 E T P R E K L K Q H S D A C K A E S G V S E E S L N K V 28

Tm13.17 31 R N G D W E D D P K L K R Q V F C V A R N A G L A T E S G E 60
 B1 44 R K G D L E D D P K L K M Q L L C I F K A L E I V A E S G E 74
 AFP-3 29 R N R E E V D D P K L K E H A F C I L K R A G F I D A S G E 58

Tm13.17 61 V V V D V L R E K V R K V T D N D E E T E K I I N K C A V K 90
 B1 75 I E A D T F K E K L T R V T N D D E E S E K I V E K C T V T 105
 AFP-3 59 F Q L D H I K T K F K E N S E H P E K V D D L V A K C A V K 88

Tm13.17 91 R D T V E E T V F N T F K C V M K N K P K F S P V D 116
 B1 106 E D T P E D T A F E V T K C V L K D K P N F F G D L F V 124
 AFP-3 89 K D T P Q H S S A D F F K C V H D N R S 108

FIG 2.12

09876343-060701

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

FIG 3.0

09876543210

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCTTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

polyadenylation signal

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAA

poly (A) tail

FIG 3.1

start



2-2 G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T G C **G**
 2-3 G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T G C **T**

2-2 T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G
 2-3 T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G

2-2 A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A
 2-3 A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A

2-2 A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C
 2-3 A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C

2-2 G A C A A A G T C C G C A C A G G T G T C T T G G T C G A **T** G A T C C C A
 2-3 G A C A A A G T C C G C A C A G G T G T C T T G G T C G A **C** G A T C C C A

2-2 A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C
 2-3 A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C

2-2 T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G
 2-3 T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G

2-2 G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G
 2-3 G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G

2-2 A A G A **G** G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A
 2-3 A A G A **A** G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A

2-2 G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C
 2-3 G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C

2-2 A A G T G T A T T T A C G A C A G **C** A A A C C T G A T T T C T C T C C T A
 2-3 A A G T G T A T T T A C G A C A G **T** A A A C C T G A T T T C T C T C C T A

2-2 T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A
 2-3 T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A

2-2 T A A A G G T A **A** T A T C G T T A T G **T** A A A A A
 2-3 T A A A G G T A **C** T A T C G T T A T G **A** A A A A A

FIG. 3.2

09876348-060701

Predicted Amino Acid

Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

FIG 3.3

096348-060701

C

FIG 3.4

09876348.060701

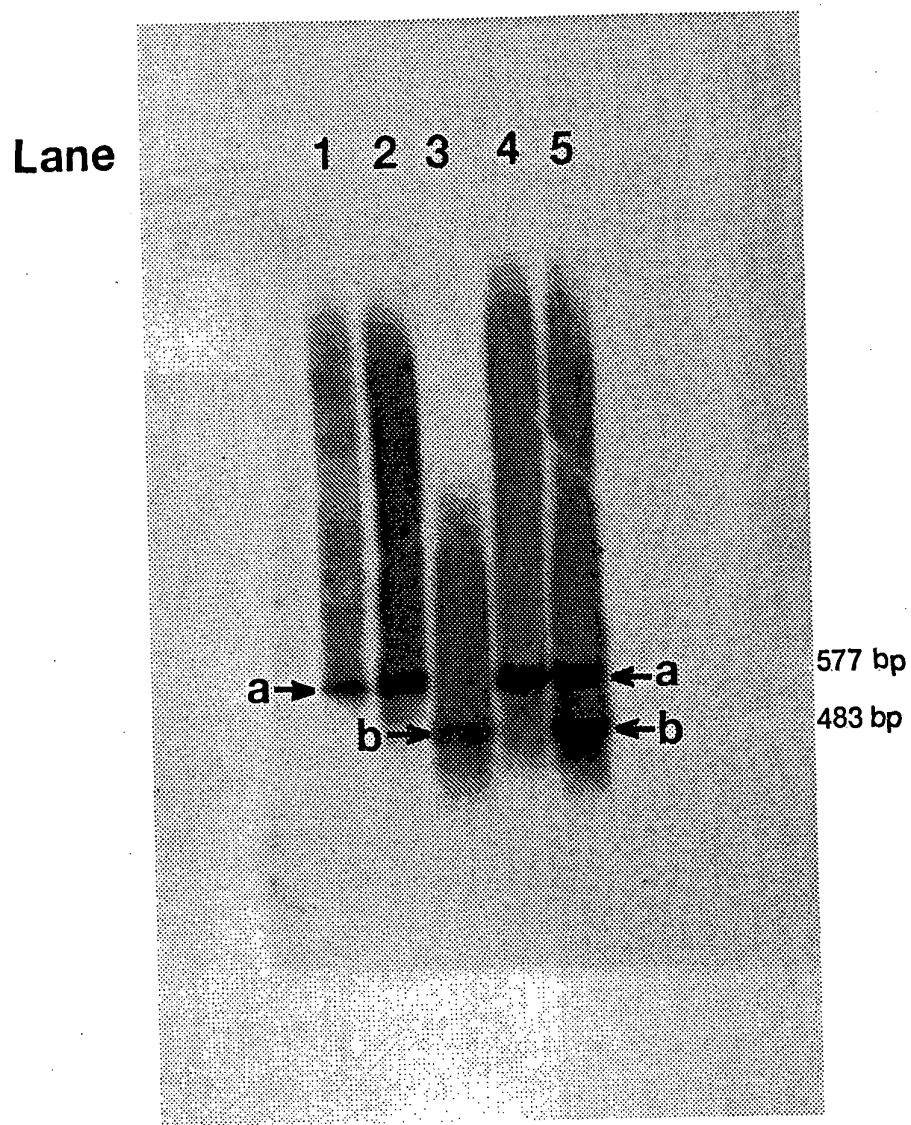


FIG 4.0

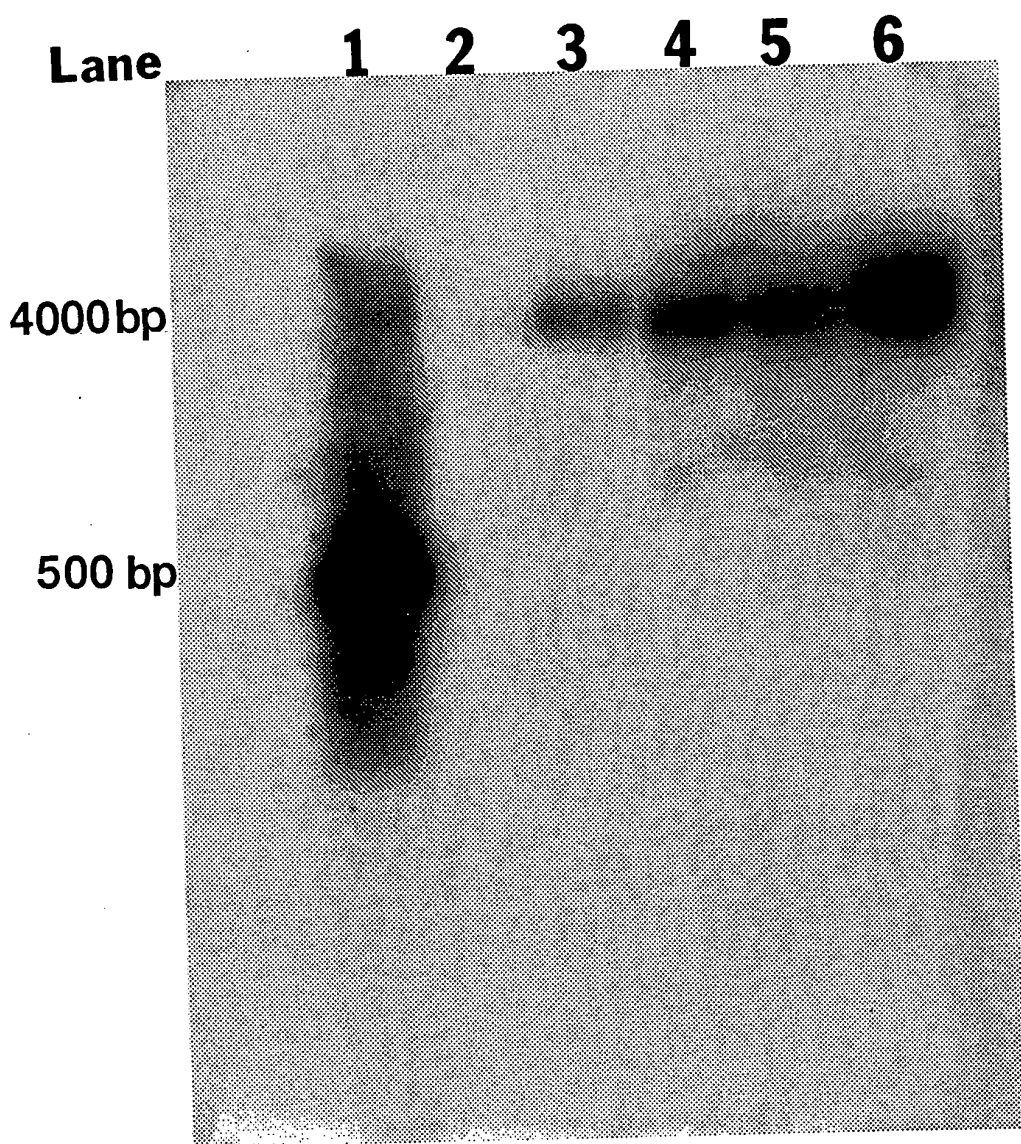


FIG 4.1

09876348-060701

Lane
4000bp
500bp

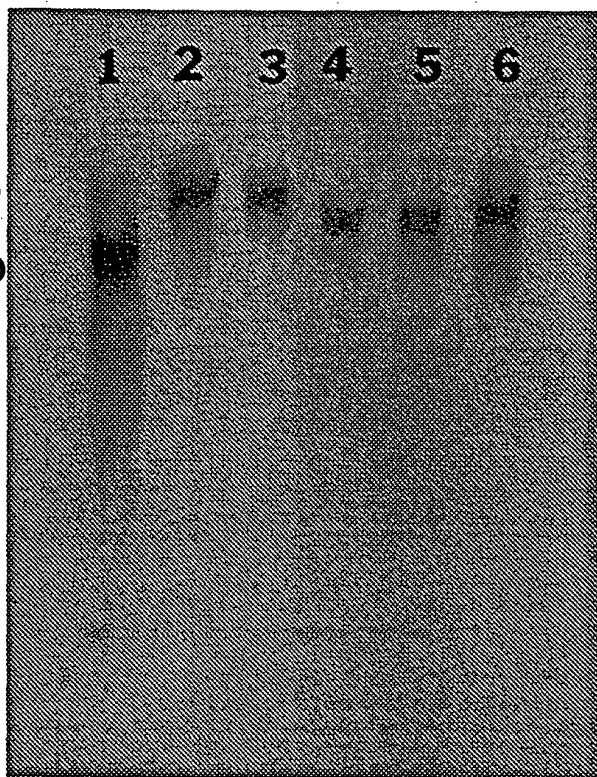
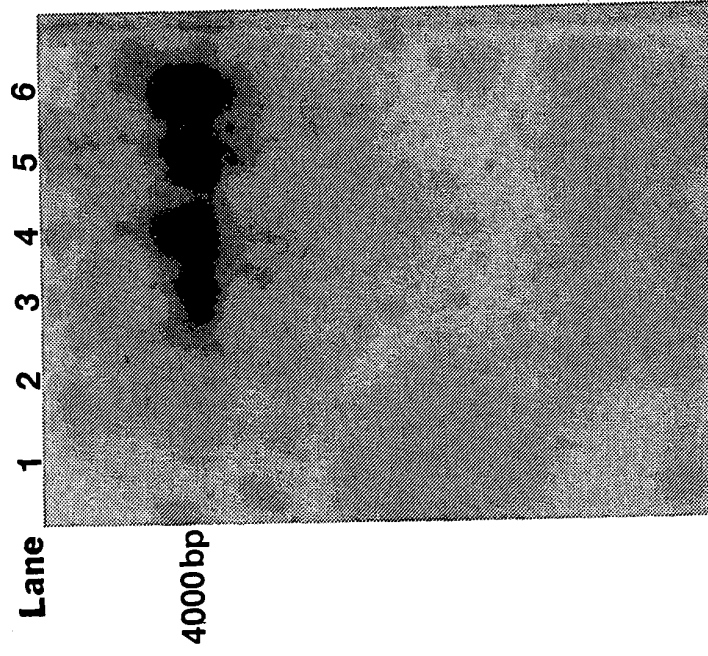


FIG 4.2

A.



B.

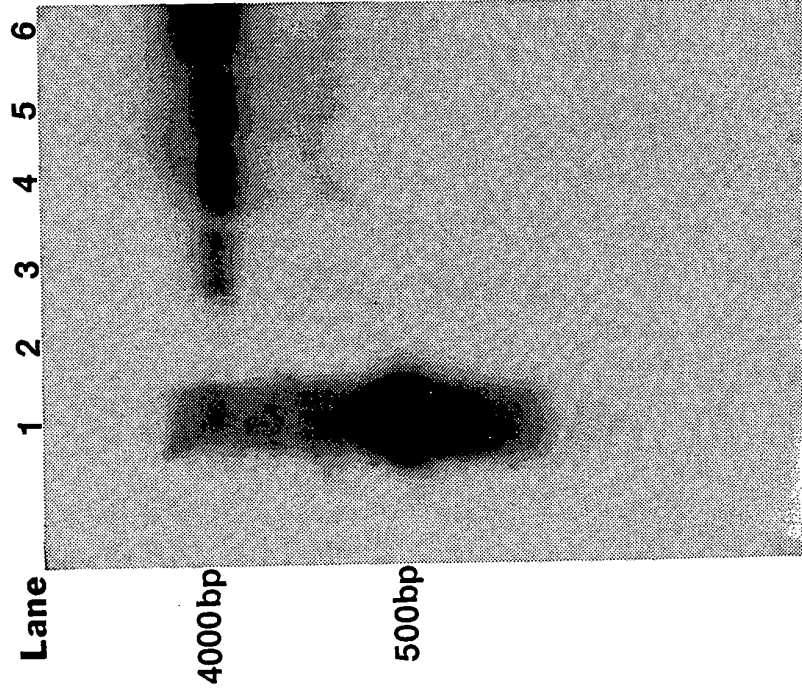


FIG 4.3

09876345060708

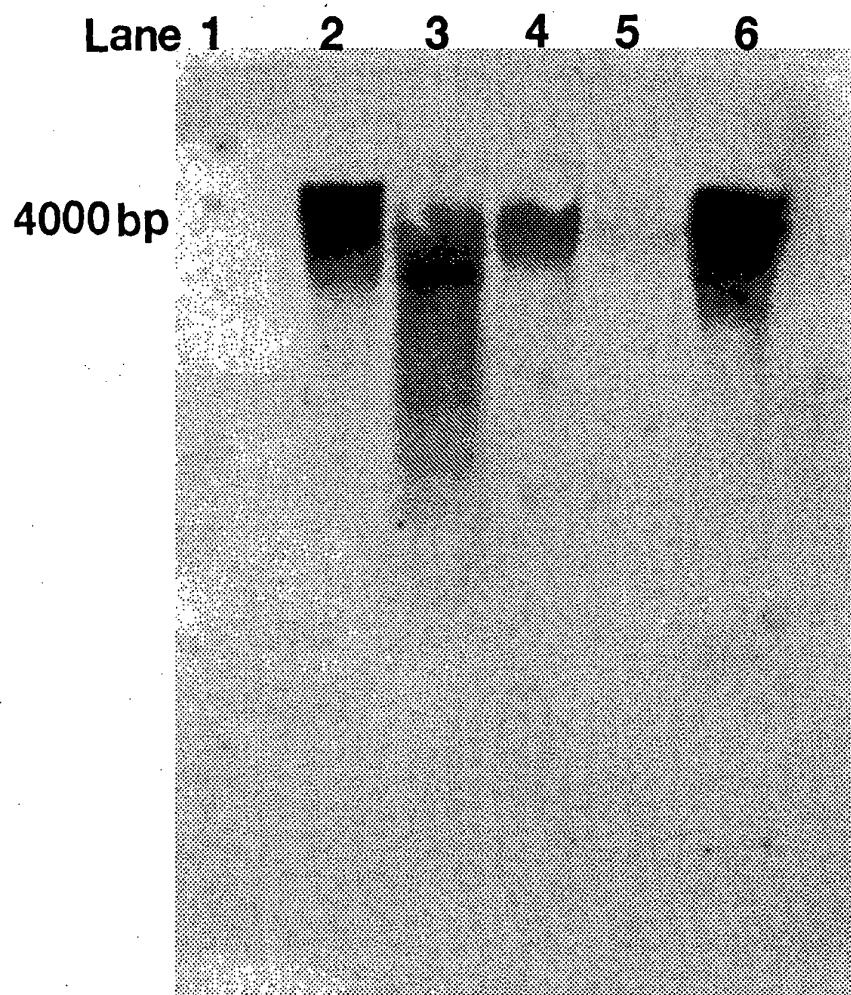
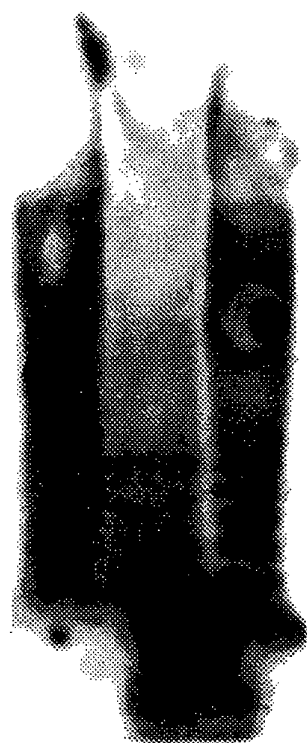


FIG 4.4

09876348-060704

Lane 1 2 3 4 5



23130

9416

4361

2322

2027

564

FIG 4.5

[illegible]

FIG. 4.6 a

B.

Forward Primer

2-2 LTDEQIQKRNKISKECQQVS **GVSQET** IDKVRTGVLV
 Tm 13.17 LTEAQIEKLNKISKKCCNES **GVSQEI** ITKARNGDWE
 B2 LTEEDLQLLRQTSAECKTES **GASEAV** IKKARKGDLE
 AFP-3 ETPREKLKQHSDACKAES **GVSEES** LNKVRNREEV

2-2 DDPKMKKHVLCFSKKTGVATEAGDTNVEVLKAKLKH
 Tm 13.17 DDPKLKRQVFCVARNAGLATESGEVVVDVLREKVRK
 B2 DDPKLKMQLLCIFKALEIVAESGEIEADTFKEKLTR
 AFP-3 DDPKLKEHAFCLKRAGFIDASGEFQLDHIKTKFKE

Reverse Primer

2-2 VAS DEEVDKIVQKCVVKK **ATPEET** AYDTFKCIYDS
 Tm 13.17 VTDNDEETEKIINKCAVKR **DTVEET** VFNTFKCVMKN
 B2 VTNDDEESEKIVEKCTVTE **DTPEDT** AFEVTKCVLKD
 AFP-3 NSEHPEKVDDLVAKCAVKK **DT PQHS** SADFFKCVHDN

2-2 KPDFSPI D
 Tm 13.17 KPKFSPVD
 B2 KPNFFGDLFV
 AFP-3 RS

C.

Primer	percent % composition				Melting Temperature (°C)
	A	C	G	T	
Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

FIG 4.6

09876345.060701

09876348.060701

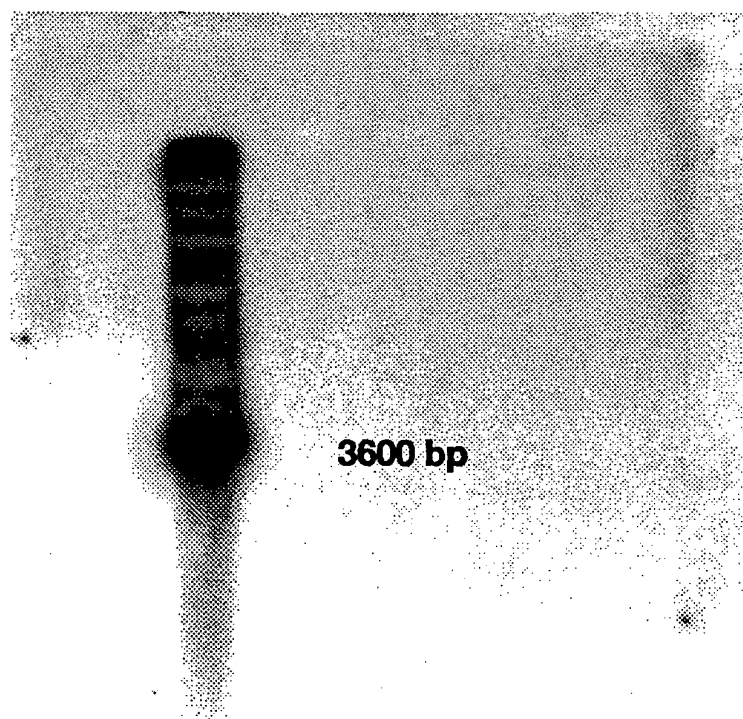


FIG 4.7

09876343-060701

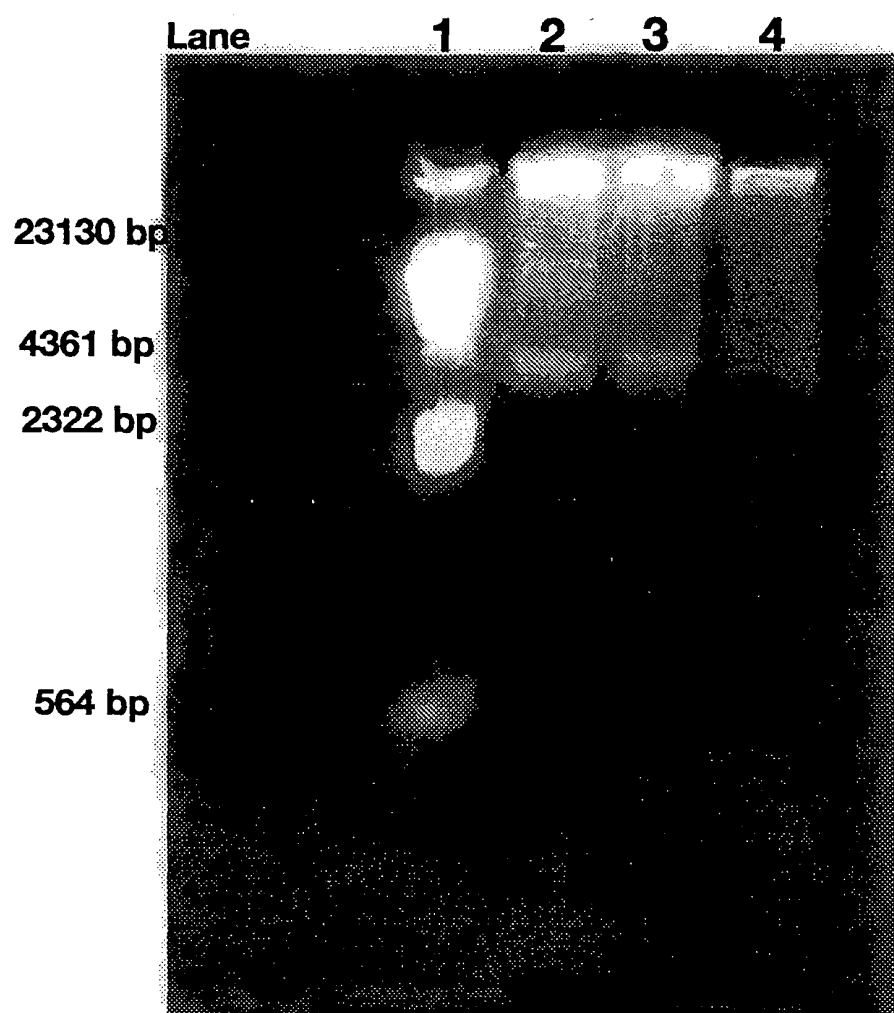


FIG 4.8

09876348.060701

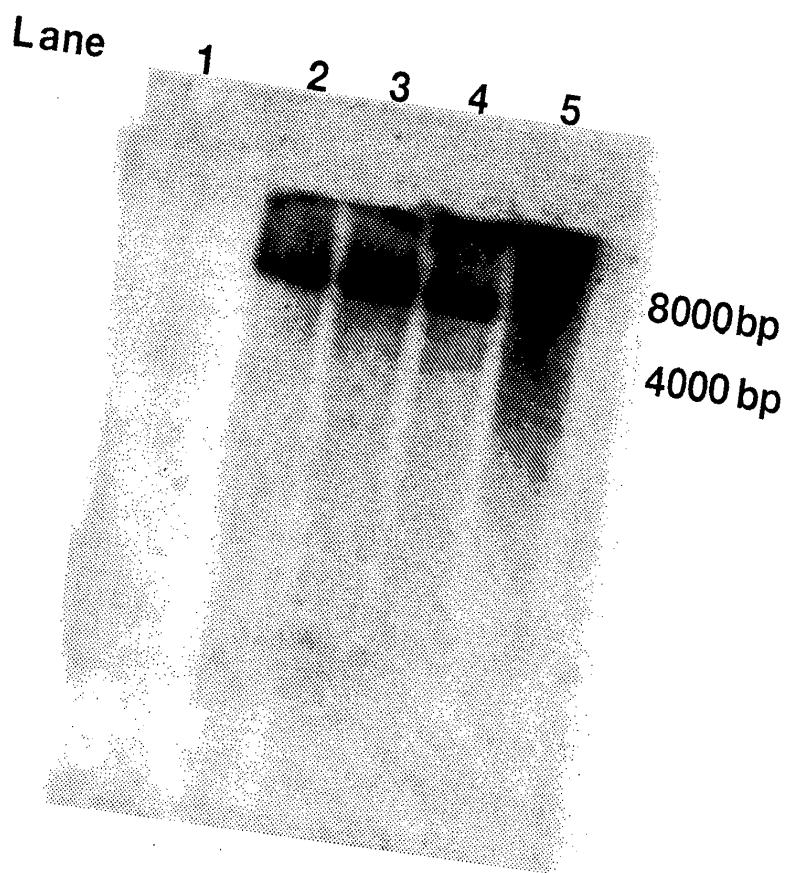


FIG 4.9

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGGTTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAA polyadenylation signal

poly (A) tail

FIG. 4.10 a

T02090-04592860

Analysis	Whole Protein
Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Predicted Amino Acid

Composition of 3-4

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AILFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

FIG. 4.10 b

10/09/09 09:49:28

1 GGCACGAGCAAAA ATGAAACTCCTCTTGCTTTGCTTTGCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGATGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGAGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAGAACTGGA
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

FIG. 4.11 a

FD-090-945296

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

FIG. 4.11 b

T04090-B4E9/860

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCGTTGCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAGTGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGGCTGAATTTTGACAATAAAGGT
I D

polyadenylation signal

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAA

poly (A) tail

FIG. 4.12 a

109676349-060701

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

FIG. 4.12 b

FOI 090-04292860



2-2	GGCA	CGAG	CAAA	AAAT	GAA	AACT	CCCT	CTTG	GTGC	TTTG	CGCC	CGCC	CAAT	CGT	CAAT	CGGA	AGCT	CAGGC
2-3	GGCA	CGAG	CAAA	AAAT	GAA	AACT	CCCT	CTTG	GTGC	TTTG	CGCC	CGCC	CAAT	CGT	CAAT	CGGA	AGCT	CAGGC
3-4	GGCA	CGAG	CAAA	AAAT	GAA	AACT	CCCT	CTTG	GTGC	TTTG	CGCC	CGCC	CAAT	CGT	CAAT	CGGA	AGCT	CAGGC
7-5	GGCA	CGAG	CAAA	AAAT	GAA	AACT	CCCT	CTTG	GTGC	TTTG	CGCC	CGCC	CAAT	CGT	CAAT	CGGA	AGCT	CAGGC
2-2	TCT	CAAC	CGGA	CGGA	CAAA	TACA	GAA	AAAG	GAAC	CAAG	ATCA	GCA	AAAG	ATGG	CCCA	AGCA	GGGT	CCGGA
2-3	TCT	CAAC	CGGA	CGGA	CAAA	TACA	GAA	AAAG	GAAC	CAAG	ATCA	GCA	AAAG	ATGG	CCCA	AGCA	GGGT	CCGGA
3-4	TCT	CAAC	CGGA	CGGA	CAAA	TACA	GAA	AAAG	GAAC	CAAG	ATCA	GCA	AAAG	ATGG	CCCA	AGCA	GGGT	CCGGA
3-9	TCT	CAAC	CGGA	CGGA	CAAA	TACA	GAA	AAAG	GAAC	CAAG	ATCA	GCA	AAAG	ATGG	CCCA	AGCA	GGGT	CCGGA
7-5	TCT	CAAC	CGGA	CGGA	CAAA	TACA	GAA	AAAG	GAAC	CAAG	ATCA	GCA	AAAG	ATGG	CCCA	AGCA	GGGT	CCGGA
2-2	GTCC	CAAG	AGAC	CGAT	TCGA	CAAA	AGT	CCGC	ACAC	AGGT	GTCT	TTGG	TCGA	TTGG	TCGA	AAAT	TGAA	AGAA
2-3	GTCC	CAAG	AGAC	CGAT	TCGA	CAAA	AGT	CCGC	ACAC	AGGT	GTCT	TTGG	TCGA	TTGG	TCGA	AAAT	TGAA	AGAA
3-4	GTCC	CAAG	AGAC	CGAT	TCGA	CAAA	AGT	CCGC	ACAC	AGGT	GTCT	TTGG	TCGA	TTGG	TCGA	AAAT	TGAA	AGAA
3-9	GTCC	CAAG	AGAC	CGAT	TCGA	CAAA	AGT	CCGC	ACAC	AGGT	GTCT	TTGG	TCGA	TTGG	TCGA	AAAT	TGAA	AGAA
7-5	GTCC	CAAG	AGAC	CGAT	TCGA	CAAA	AGT	CCGC	ACAC	AGGT	GTCT	TTGG	TCGA	TTGG	TCGA	AAAT	TGAA	AGAA
2-2	CGTC	CTCT	GTGC	TTCT	CGAA	AGAA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA
2-3	CGTC	CTCT	GTGC	TTCT	CGAA	AGAA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA
3-4	CGTC	CTCT	GTGC	TTCT	CGAA	AGAA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA
3-9	CGTC	CTCT	GTGC	TTCT	CGAA	AGAA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA
7-5	CGTC	CTCT	GTGC	TTCT	CGAA	AGAA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA	AACT	GGCA	AGTG	GGCA
2-2	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC
2-3	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC
3-4	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC
3-9	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC
7-5	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC	CAAG	CGCA	AGCT	GAAG	CAAT	GTGC
2-2	CAAG	AGCG	CCAC	CAAC	CAAG	AGGA	AAAG	GGCT	TTAT	GACA	CACT	TTCA	AGGT	TTCA	AGGT	TTCA	AGGT	TTCA
2-3	CAAG	AGCG	CCAC	CAAC	CAAG	AGGA	AAAG	GGCT	TTAT	GACA	CACT	TTCA	AGGT	TTCA	AGGT	TTCA	AGGT	TTCA
3-4	CAAG	AGCG	CCAC	CAAC	CAAG	AGGA	AAAG	GGCT	TTAT	GACA	CACT	TTCA	AGGT	TTCA	AGGT	TTCA	AGGT	TTCA
3-9	CAAG	AGCG	CCAC	CAAC	CAAG	AGGA	AAAG	GGCT	TTAT	GACA	CACT	TTCA	AGGT	TTCA	AGGT	TTCA	AGGT	TTCA
7-5	CAAG	AGCG	CCAC	CAAC	CAAG	AGGA	AAAG	GGCT	TTAT	GACA	CACT	TTCA	AGGT	TTCA	AGGT	TTCA	AGGT	TTCA
2-2	TTTC	CTCT	CTAT	TTGA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA
2-3	TTTC	CTCT	CTAT	TTGA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA
3-4	TTTC	CTCT	CTAT	TTGA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA
3-9	TTTC	CTCT	CTAT	TTGA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA
7-5	TTTC	CTCT	CTAT	TTGA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA
2-2	GTAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA
2-3	GTAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA
3-4	GTAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA
3-9	GTAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA
7-5	GTAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA

FIG. 413



2-2	MK	LL	LL	CF	FA	FA	AI	VI	GA	QA	LT	DE	QI	QK	RN	KI	SK	EC	QQ	V	SG	V	SQ	ET	I	DK	VR	TG	VL	V
2-3	MK	LL	LL	CF	FA	FA	AI	VI	GA	QA	LT	DE	QI	QK	RN	KI	SK	EC	QQ	V	SG	V	SQ	ET	I	DK	VR	TG	VL	V
3-4	MK	LL	LL	CF	FA	FA	AI	VI	GA	QA	LT	DE	QI	QK	RN	KI	SK	EC	QQ	V	SG	V	SQ	ET	I	DK	VR	TG	VL	V
3-9	MK	LL	LL	CF	FA	FA	AI	VI	GA	QA	LT	DE	QI	QK	RN	KI	SK	EC	QQ	E	SG	V	SQ	ET	I	DK	VR	TG	VL	V
7-5	MK	LL	LL	CF	FA	FA	AI	VI	GA	QA	LT	DE	QI	QK	RN	KI	SK	EC	QQ	V	SG	V	SQ	ET	I	DK	VR	TG	VL	V

2-2	DD	PK	MM	KK	HH	V	L	CF	SK	KT	GV	AT	EA	GD	TN	VE	V	L	KA	KL	KH	V	AS	DE	EE	V	DK	I	V	QK	CV	V	KK	
2-3	DD	PK	MM	KK	HH	V	L	CF	SK	KT	GV	AT	EA	GD	TN	VE	V	L	KA	KL	KH	V	AS	DE	EE	V	DK	I	V	QK	CV	V	KK	
3-4	DD	PK	MM	KK	HH	V	L	CF	SK	KT	GV	AT	EA	GD	TN	VE	V	L	KA	KL	KH	V	AS	DE	EE	V	DK	I	V	QK	CV	V	KK	
3-9	DD	PK	MM	KK	HH	V	L	CF	SK	R	KT	GV	AT	EA	GD	TN	VE	V	L	KA	KL	KH	V	AS	DE	EE	V	DK	I	V	QK	CV	V	KK
7-5	DD	PK	MM	KK	HH	V	L	CF	SK	KT	GV	AT	EA	GD	TN	VE	V	L	KA	KL	KH	V	AS	DE	EE	V	DK	I	V	QK	CV	V	KK	

2-2	AT	PE	ET	AY	DT	FF	K	CI	Y	DS	K	P	D	F	S	P	I	D	*	
2-3	AT	PE	ET	AY	DT	FF	K	CI	Y	DS	K	P	D	F	S	P	I	D	*	
3-4	AT	PE	ET	AY	DT	FF	V	K	CI	Y	DS	K	P	D	F	S	P	I	D	*
3-9	AT	PE	ET	AY	DT	FF	K	CI	Y	DS	K	P	D	F	S	P	I	D	*	
7-5	AT	PE	ET	AY	DT	FF	K	CI	Y	DS	K	P	D	F	S	P	I	D	*	

FIG. 4.14

	(kDa)	(% mole)																					
		MW	AA	Cys	Pro	Phe	Ile	Val	Met	Leu	% most hydrophobic	Gly	Ala	Tyr	His	Trp	Asx	Glx	Arg	Lys	Ser	Thr	% most hydrophilic
Tm	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3	57.3	
12.86																							
Tm	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.4	0	0	7.12	15.6	3.31	6.14	32.14	
13.17															1								
2-2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23	
2-3	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23	
3-4	12.84	115	2.41	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.09	32.24	
3-9	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07	32.38	
7-5	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23	

FIG. 4.15

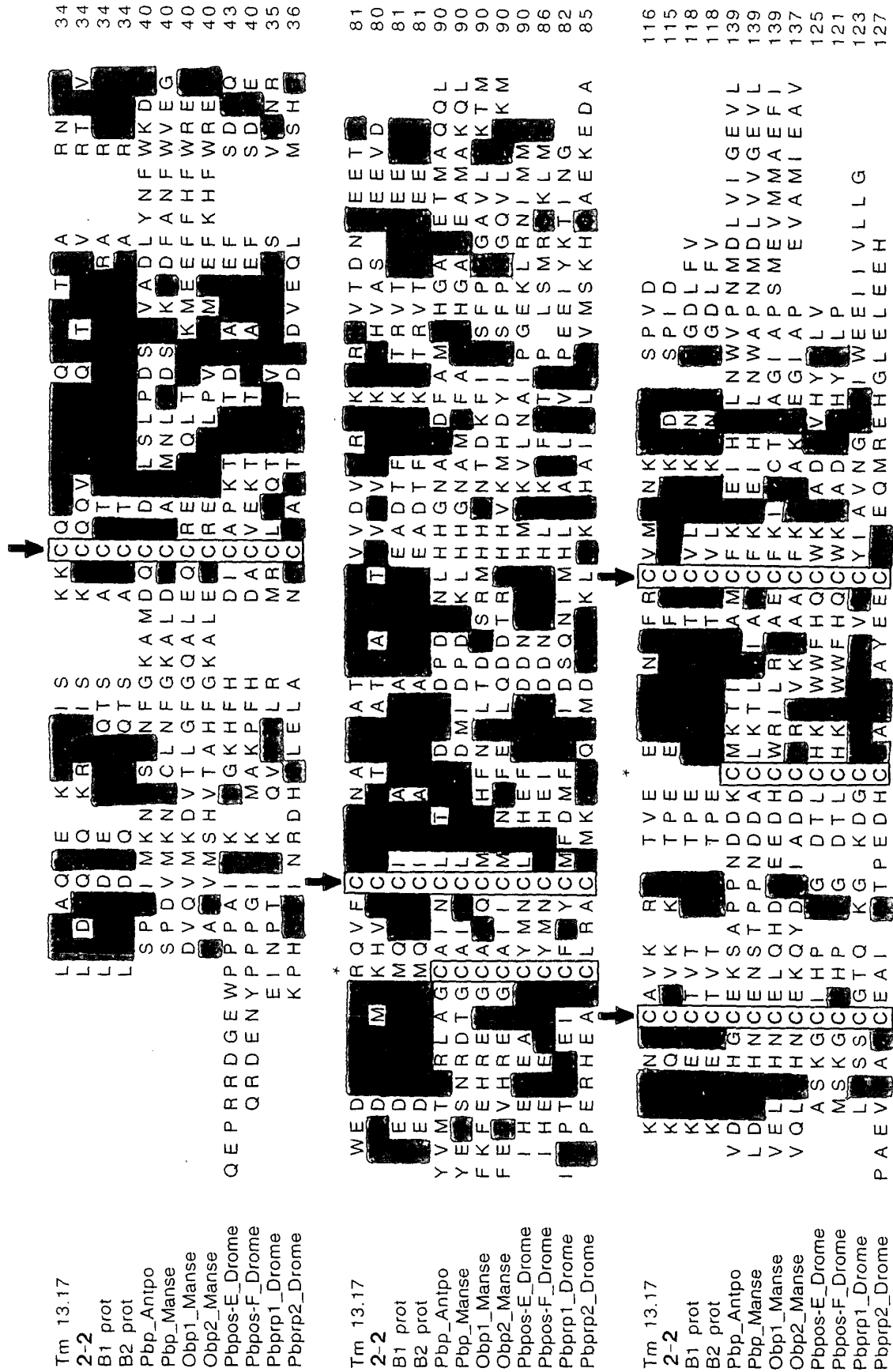
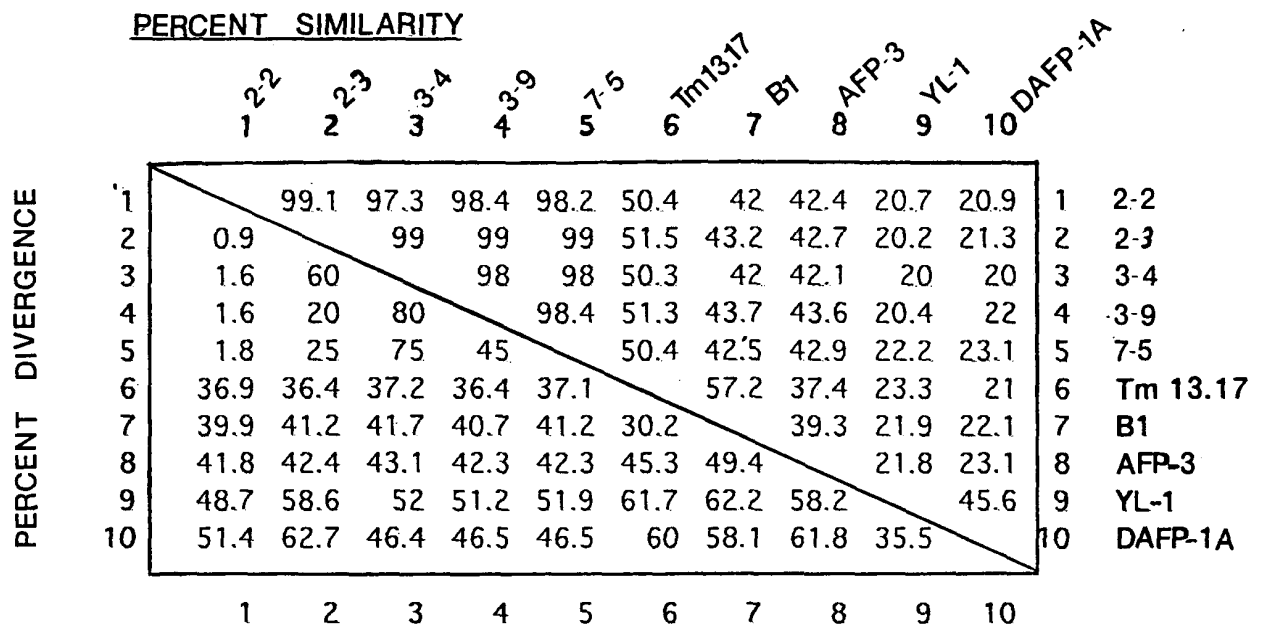


FIG. 4.17

NUCLEOTIDE SEQUENCES



AMINO ACID SEQUENCES

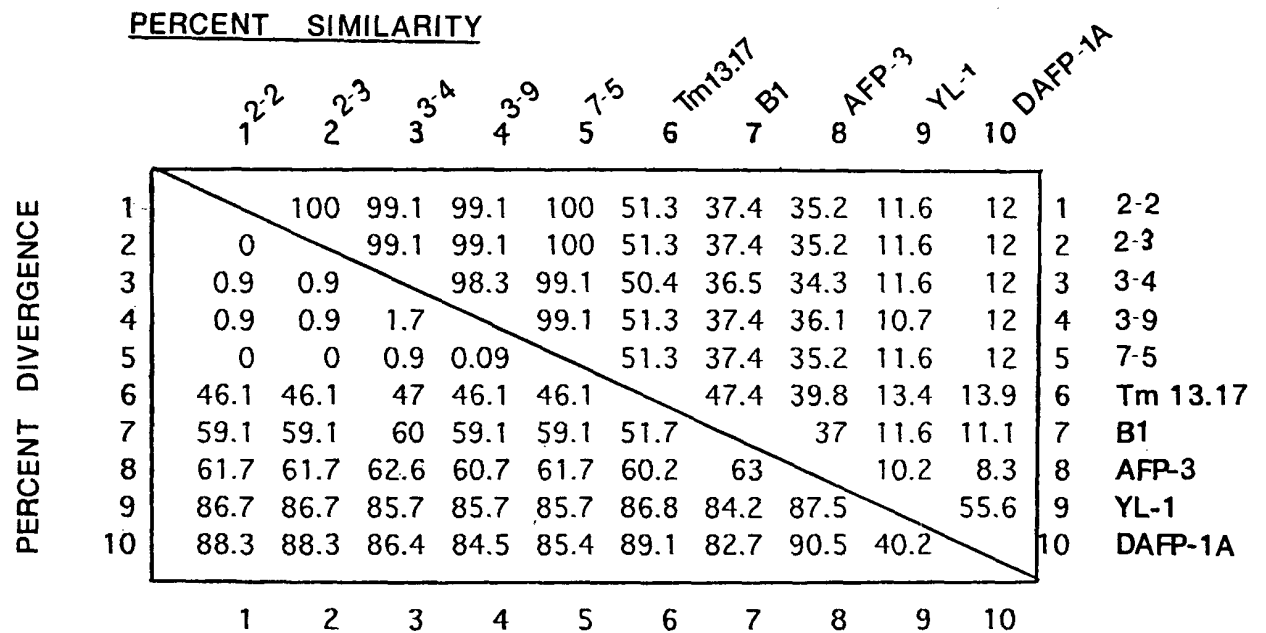


FIG 4.19

09076348-060701

09876348-060701

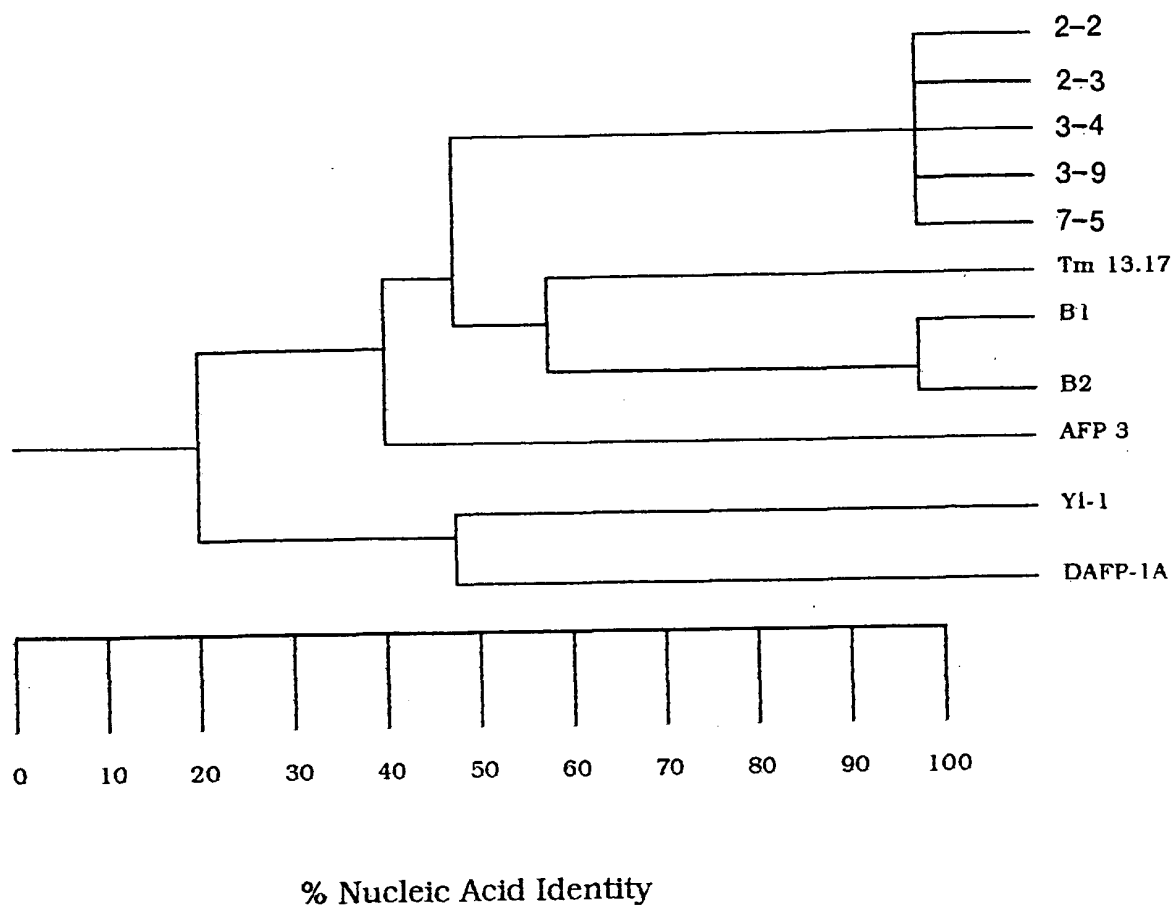


FIG 4.20

Table 1. Mean values of the variables measured during the 60-min test

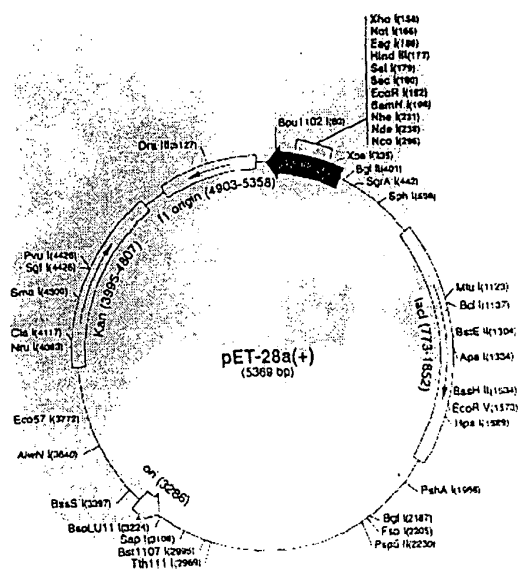


FIG. 5.0

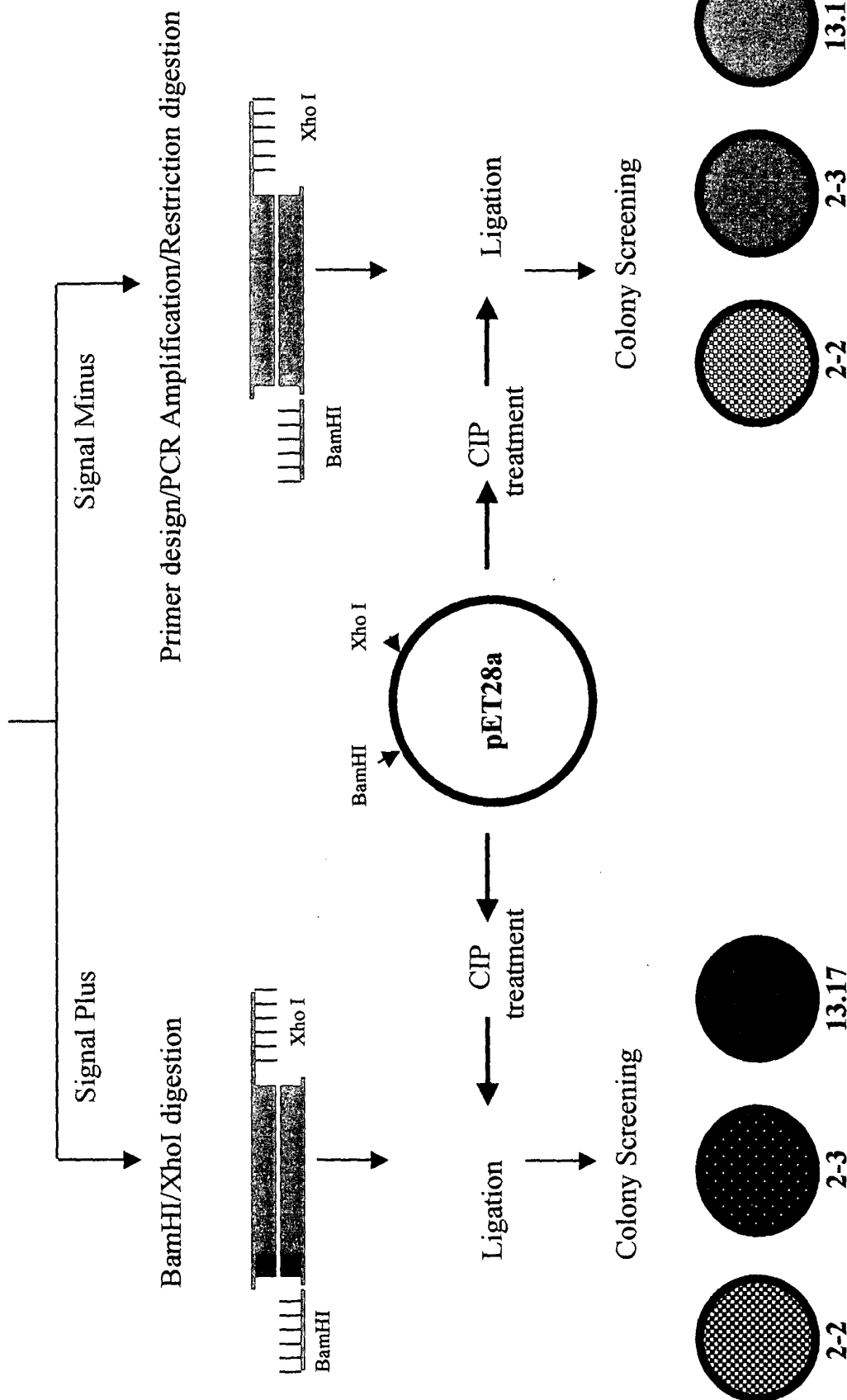
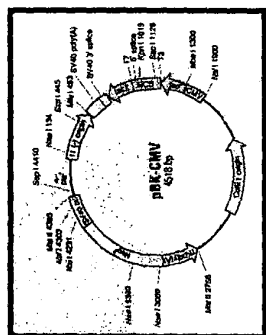


FIG. 5.1

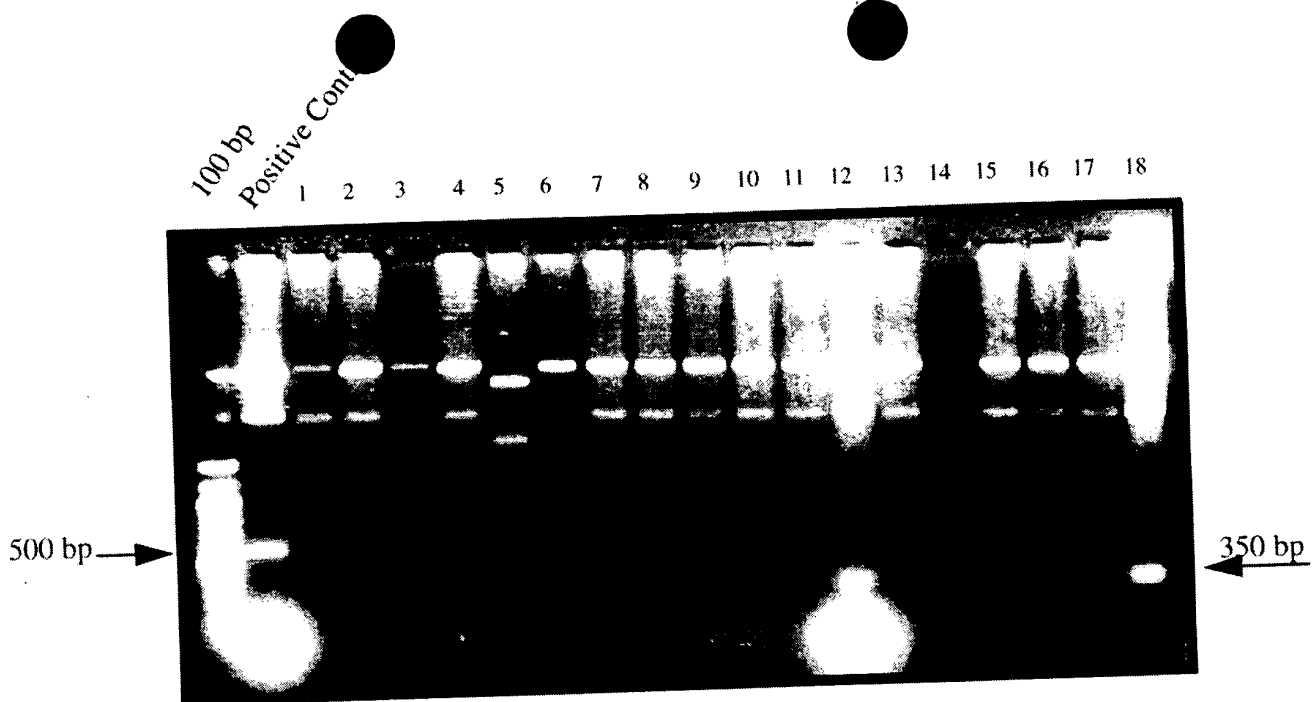


FIG. 5.2

102090" 84E92B60

10/20/90 04:34:00

650 bp

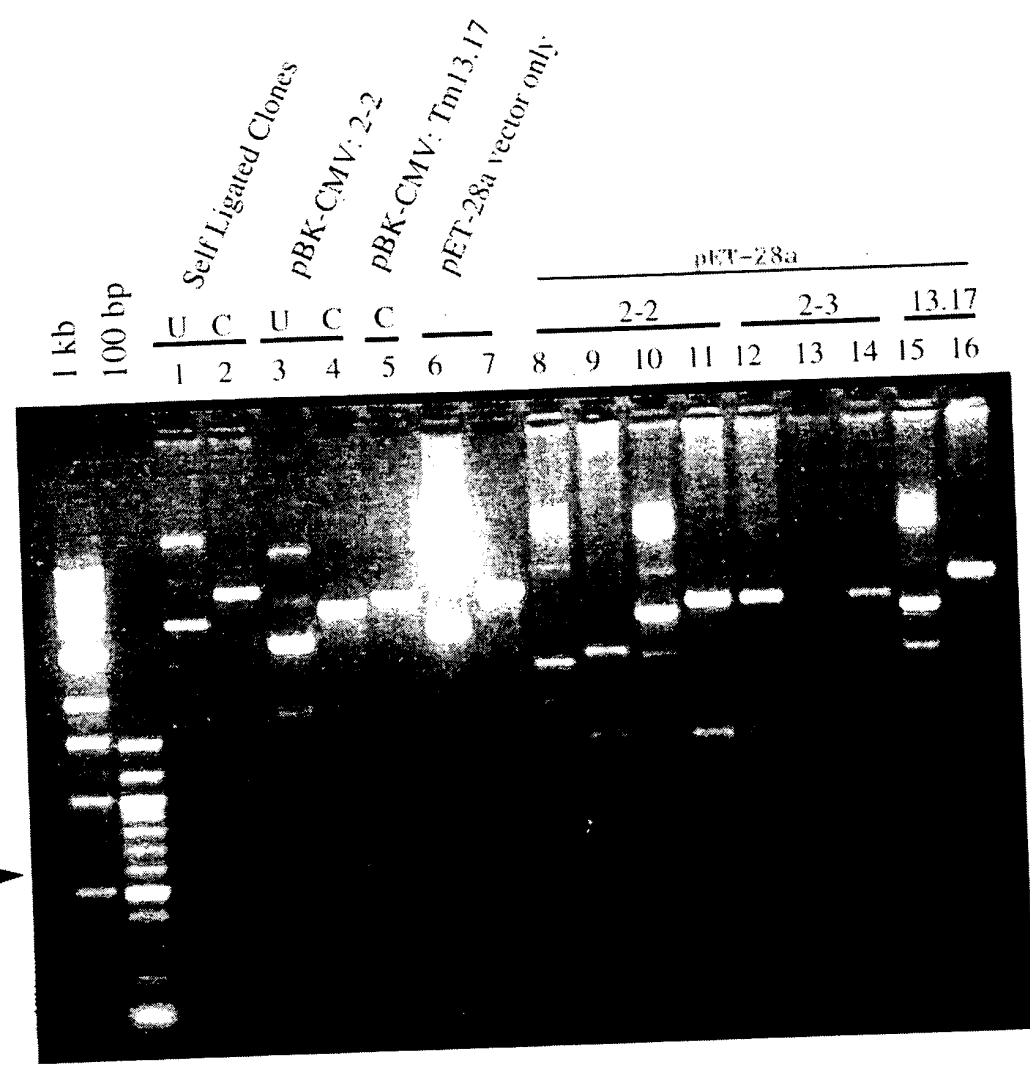


FIG. 5.3

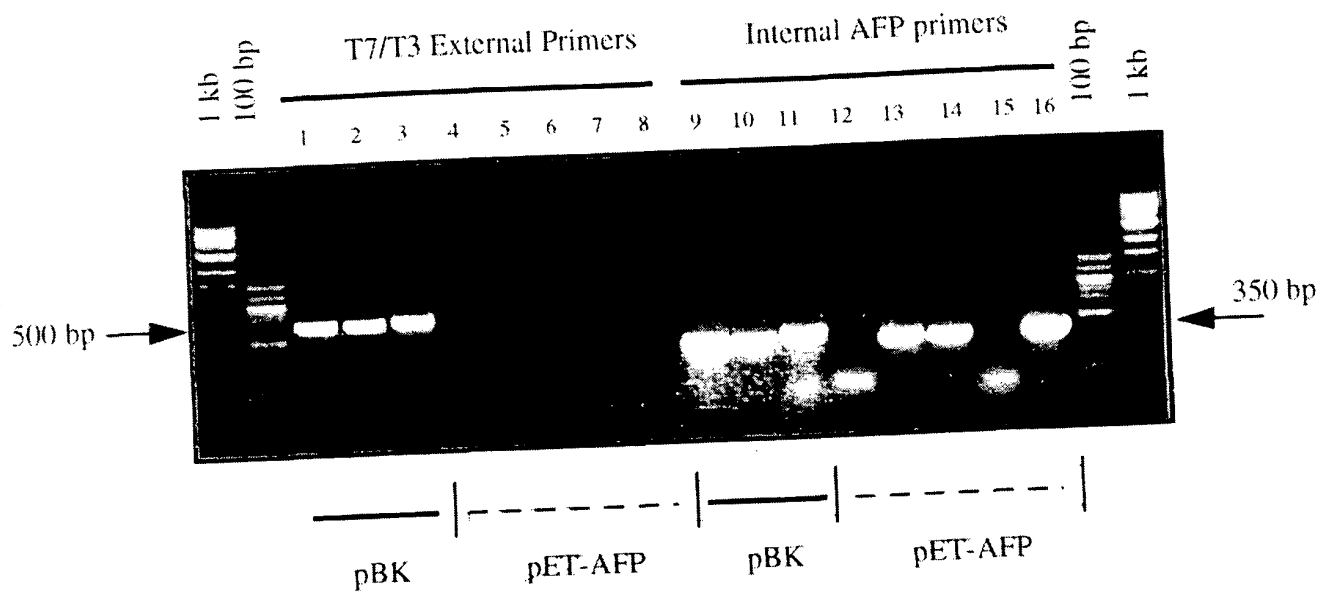


FIG. 5.4

09876348 060701

09876345-060701

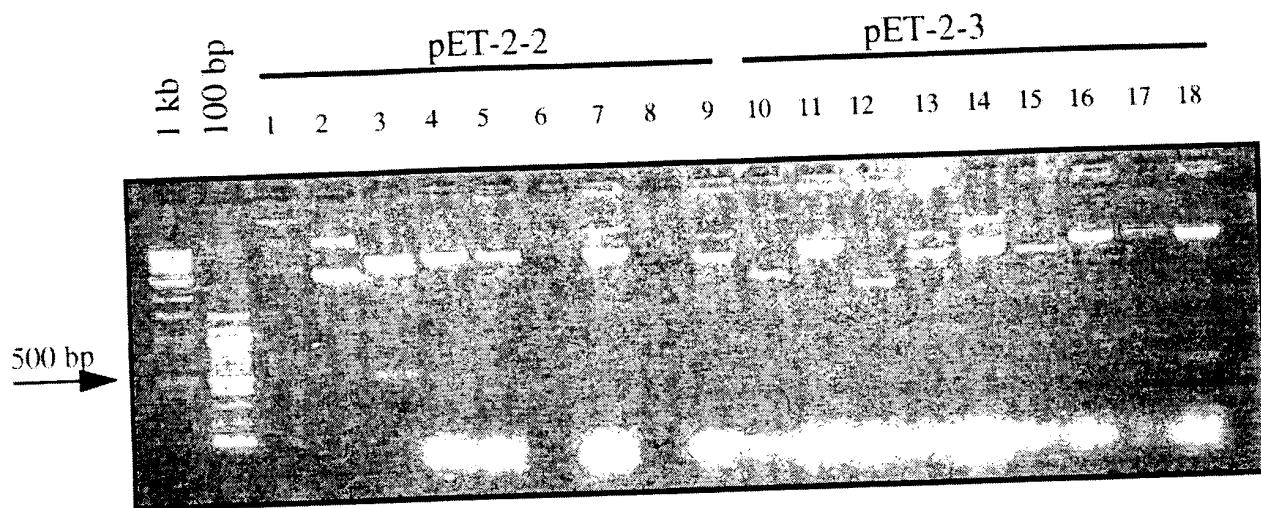


FIG. 5.5

[illegible]

2-2 S+ 2-2S- 2-3S+ 2-3S- 13.17S+ 13.17S-

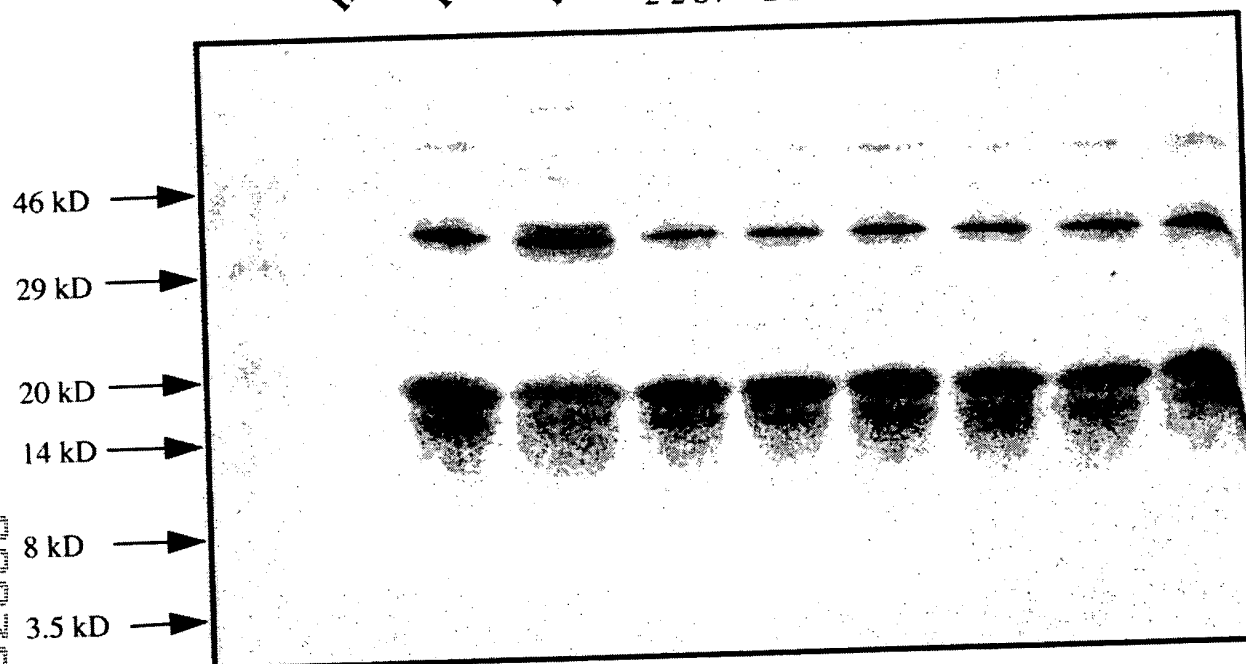


FIG. 5.6

His-tagged Clone 2.2 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AFP Start Codon	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
N-terminal of mature AFP	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
Stop Codon	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGT	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
Polyadenylation signal Poly-A tail	
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

FIG. 5.7

His-tagged clone 2.2 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

FIG. 5.8

09876340-060701

His-tagged clone 2.3 with signal sequence

TTGTTAGCGG ATGGAATCC CTCGTAGGGG ATAATTTTGT TTA	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
AFP Start Codon	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
N-terminal of Mature AFP	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
Stop Codon	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGT	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
Polyadenylation signal Poly-A tail	
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA	645
AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	682

FIG. 5.9

His-tagged Clone 2.3 without signal sequence

TTGTTAGCGG ATGGAATTC CTCGTAGGGG ATAATTTTGT TTA	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

FIG. 5.10

His-tagged Tm 13.17 with signal sequence

TTGTTAGCGG ATGGAATCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His Ser	
-65 -60 -55	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-50 -45 -40	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile	
-35 -30 -25	
AFP Start Codon	
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC	231
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser	
-20 -15 -10	
N-terminal of mature AFP	
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT	276
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile	
-5 1 5	
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA	321
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly	
10 15 20	
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG	366
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu	
25 30 35	
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC	411
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn	
40 45 50	
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG	456
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu	
55 60 65	
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG	501
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu	
70 75 80	
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG	546
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu	
85 90 95	
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG	595
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys	
100 105 110	
Stop Codon	
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG	643
Phe Ser Pro Val Asp *	
115	
Polyadenylation signal Poly-A tail	
TGTGCTTTAC ATATAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAAA	693
AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT	777

FIG. 5.11

His-tagged Tm 13.17 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA	186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	
-5 1 5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG	231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT	276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	
25 30 35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT	321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	
40 45 50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG	366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	
55 60 65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC	411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	
70 75 80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG	456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	
85 90 95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA	501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	
100 105 110	
Stop Codon	
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Val Asp *	
115	

FIG. 5.12

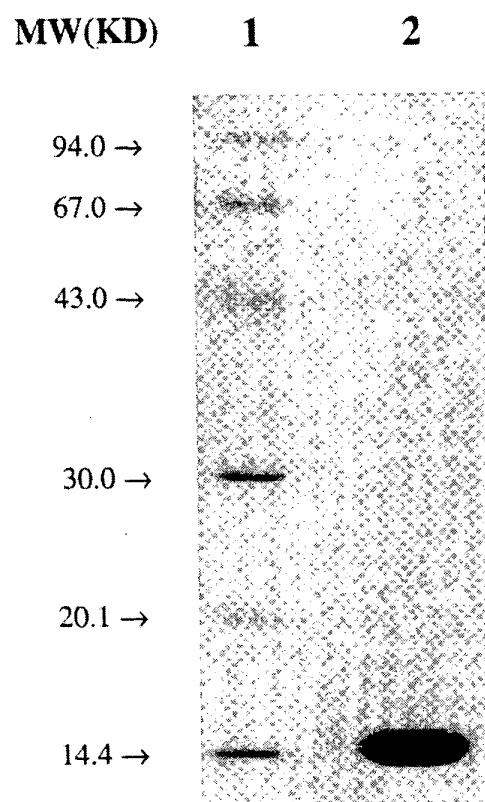


FIG. 6.0



FIG. 6.1

09876348-050701

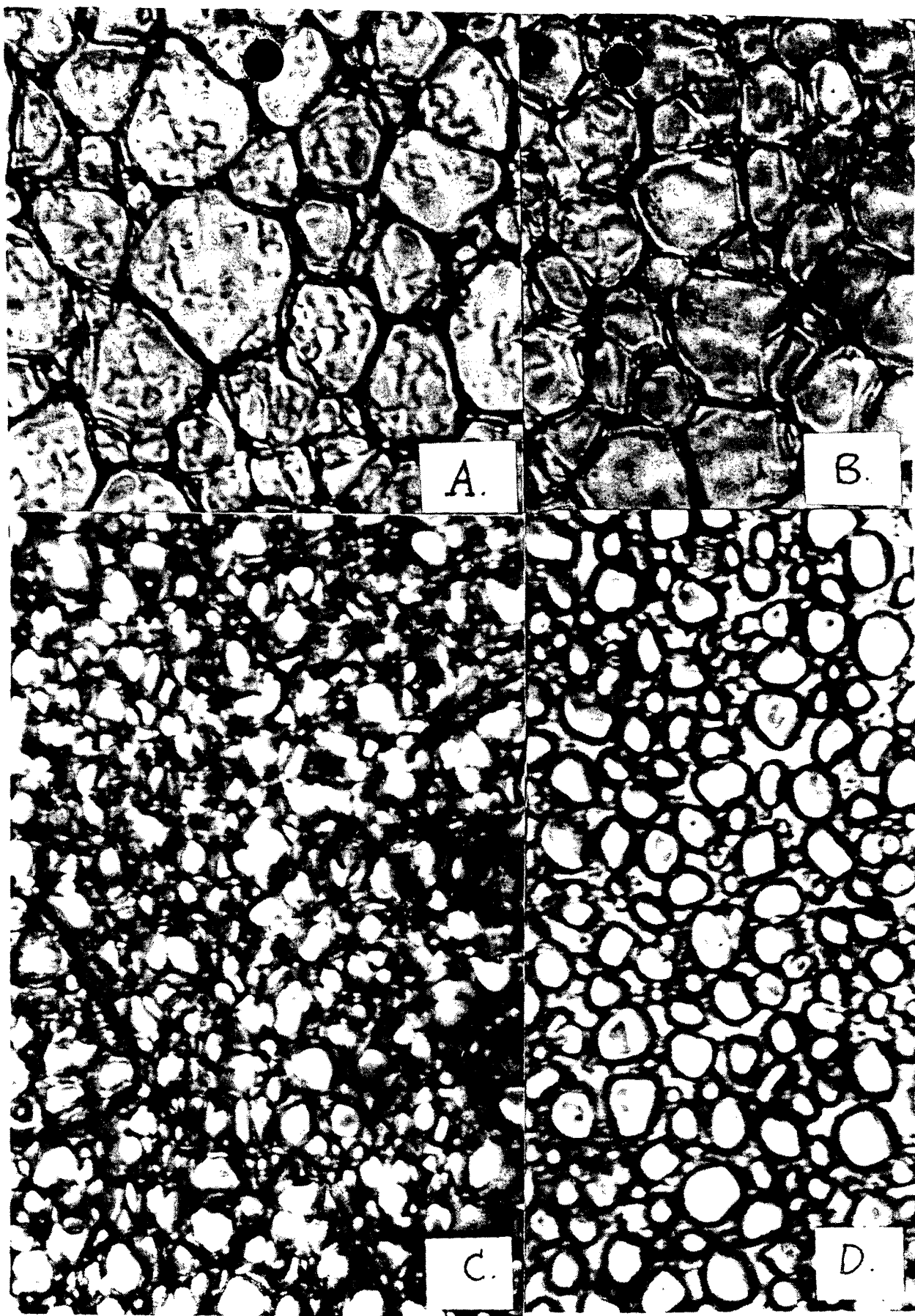


FIG. 6.2

FOI b7E b7C b7D

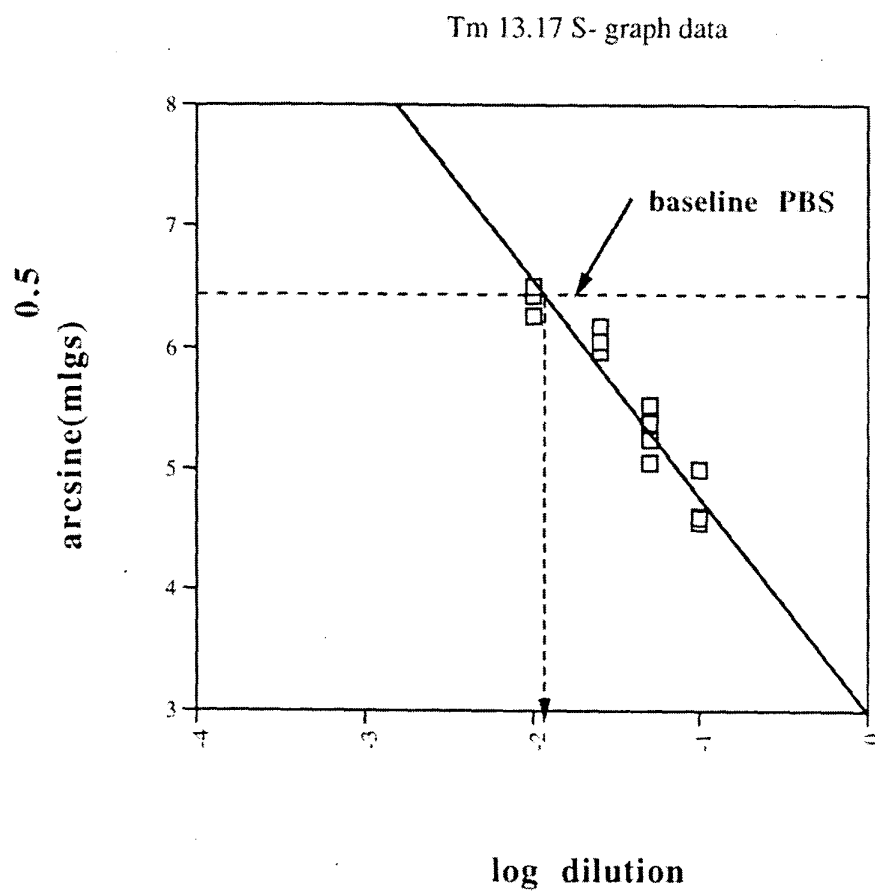


FIG. 6.3

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulfhydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulfhydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

FIG. 7.1

[illegible]

FIG. 7.2

	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
118	C	C	C	C	C	C	C	N	A	N		N
119	A	A	A	A	A	A	A	A	C	N	G	N
120	G	G	G	G	G	G	G	N	T	N	T	N
121	G	G	G	G	G	G	G	N	G	N	G	N
122	T	T	T	T	T	T/A	T	T/A	G	T/A	A	A/T
123	G	G	G	G	G	G	G	R	A	R	G	R
124	T	T	T	T	T	T	T	T/A	A	T/A	T	T/A
125	C	C	C	C	C	C	C	C/G	G	C/G	C	C/G
126	C	C	C	C	C	C	C	Y	T	Y	T	Y
127	G	G	G	G	G	G	G	G	G	G	G	G
128	G	G	G	G	G	G	G	G	G	G	G	G
129	A	A	A	A	A	A	A	G	G	A	A	A
130	O	G	T	T	G	G	T	G	T	T	T	T
131	T	T	T	T	T	T	T	T	T	T	T	T
132	G	T	G	T	G	T	G	G	T	G	T	R
133	T	T	T	T	T	T	T	T	T	T	T	T
134	C	C	C	C	C	C	C	T	C	T	C	C
135	C	C	C	C	C	C	C	C/G	C	C/G	T	C
136	C	C	C	C	C	C	C	C	G	C/G	G	C/G
137	A	A	A	A	A	A	A	A	A	A	A	A
138	A	A	A	A	A	A	A	A	A	A	A	A
139	A	G	A	A	A	A	A	G	A	A	G	A
140	A	G	A	A	A	A	A	A	A	A	A	A
141	A	G	A	A	A	A	A	G	A	A	A	A
142	A	C	A	A	A	A	A	A	C	A	A	A
143	A	C	A	A	A	A	A	A	G	A	A	A
144	G	G	C	C	C	C	A	A	C	G	T	N
145	A	A	A	A	A	A	A	Y	T	R	C	Y
146	T	T	A	A	A	A	A	G/C	A	G/C	C	G/C
147	C	C	C	C	C	C	C	A	A	A	T	A
148	G	A	C	C	C	C	A	N	A	N	C	N
149	C	C	C	C	C	C	C	R	A	N	A	N
150	A	C	A	A	A	A	C	N	A	C	A	A
151	A	A	A	A	A	A	A	C	G	C/G	C	C/G
152	A	A	A	A	A	A	A	A	A	A	A	A
153	A	A	A	A	A	A	A	A	A	A	A	A
154	A	G	A	A	A	A	A	G	A	R	R	R
155	G	T	G	G	G	G	G	O	G	A	G	G
156	T	C	C	C	C	C	T	Y	C	Y	T	Y
157	C	C	C	C	C	C	T	Y	C	Y	C	C
158	C	C	C	C	C	C	G	G	C	G	C	C
159	C	C	C	C	C	C	C	C	C	C	C	C
160	A	C	A	A	A	A	A	A	A	A	A	A
161	C	A	C	A	A	A	A	N	A	A	A	A
162	A	G	A	A	A	A	A	N	A	N	C	N
163	G	G	G	G	G	G	G	G	G	N	C	C
164	G	G	T	T	T	T	T	G	G	G	G	G
165	T	T	T	T	T	T	T	T	T	T	T	T
166	G	T	G	G	G	G	G	T	G	T	G	T
167	T	C	T	T	T	T	T	A	A	T/A	A	T/A
168	C	T	C	C	C	C	C	C	C	C	A	N
169	T	T	T	T	T	T	T	T	T	T	A	N
170	G	G	G	G	G	G	G	N	G	N	A	N
171	G	G	G	G	G							

FIG. 7.2 Cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
236	A	A	A	A	A	A	A	A	A	A	C	N
237	A	A	A	A	A	A	A	A	A	A	N	N
238	A	A	A	A	A	A	A	A	A	A	C	N
239	C	C	C	C	C	C	C	C	C	C	G	C/G
240	C	C	C	C	C	C	C	C/G	C	C/G	T	N
241	G	G	G	G	G	G	G	G	G	G	G	G
242	A	A	A	A	A	A	A	A	A	A	T	G
243	A	A	A	A	A	A	A	A	A	A	A/T	A
244	A	A	A	A	A	A	A	A	A	A	G	G
245	A	A	A	A	A	A	A	A	A	A	A	A
246	C	C	C	C	C	C	C	C/G	A	A	N	N
247	A	A	A	A	A	A	A	R	Y	Y	T	Y
248	C	C	C	C	C	C	C	C/G	T	T	C	N
249	C	C	C	C	C	C	C	R	G	R	C	N
250	A	A	A	A	A	A	A	G	T	G	A	N
251	A	A	A	A	A	A	A	A/T	N	N	A	A
252	T	T	T	T	T	T	T	G	T	G	C	N
253	T	T	T	T	T	T	T	G	T	G	Y	G/C
254	T	T	T	T	T	T	T	G	T	G	G	Y
255	G	G	G	G	G	G	G	G/C	G	G/C	G	G
256	G	G	G	G	G	G	G	G	G	G	G	G
257	A	A	A	A	A	A	A	A	A	A	A	A
258	A	A	A	A	A	A	A	G/C	C	C	C	G/C
259	G	G	G	G	G	G	G	G	C	C	C	N
260	T	T	T	T	T	T	T	T	C	C	A	N
261	A	A	A	A	A	A	A	T	Y	Y	C	N
262	C	C	C	C	C	C	C	T	T	T	A	N
263	T	T	T	T	T	T	T	T	T	T	T	N
264	C	C	C	C	C	C	C	C/G	T	T	C	N
265	A	A	A	A	A	A	A	A	A	A	A	A
266	A	A	A	A	A	A	A	A	A	A	A	A
267	A	A	A	A	A	A	A	R	R	R	G	R
268	G	G	G	G	G	G	G	R	R	R	A	R
269	C	C	C	C	C	C	C	G	G	G	C	R
270	C	C	C	C	C	C	C	C/G	N	C/G	G	C/G
271	C	C	C	C	C	C	C	A	A	A	A	A
272	A	A	A	A	A	A	A	A	A	A	A	A
273	G	G	G	G	G	G	G	A	G	G	A	R
274	C	C	C	C	C	C	C	C/G	T	T	T	N
275	T	T	T	T	T	T	T	G	T	T	C	G/C
276	G	G	G	G	G	G	G	A	A	A	A	A
277	A	A	A	A	A	A	A	A	A	A	A	A
278	A	A	A	A	A	A	A	R	R	R	G	N
279	G	G	G	G	G	G	G	G	G	G	A	G
280	C	C	C	C	C	C	C	N	N	N	G	N
281	T	T	T	T	T	T	T	A	A	A	A	R
282	T	T	T	T	T	T	T	N	N	N	A	N
283	G	G	G	G	G	G	G	A	A	A	A	N
284	T	T	T	T	T	T	T	G	T	T	N	N
285	G	G	G	G	G	G	G	C	C	C	C	N
286	G	G	G	G	G	G	G	R	C	C	T	N
287	C	C	C	C	C	C	C	C	Y	Y	C	N
288	A	A	A	A	A	A	A	R	R	R	G	R
289	G	G	G	G	G							

FIG. 7.2 Cont.

05376348-060701

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
354	A	A	A	A	A	A	G	R	A	R	C	N
355	A	A	A	A	A	A	A	A	C	N	C	N
356	C	C	C	C	C	C	C	C	G	C/G	C	C/G
357	G	G	G	G	G	G	G	G	C	G/C	T	N
358	C	C	C	C	C	C	T	Y	A	N	C	N
359	T	T	T	T	T	T	T	N	T	N	A	N
360	T	T	T	T	T	T	T	T	T	A	G	N
361	A	A	A	A	A	A	T	A	T	C	C	N
362	T	T	T	T	T	T	C	T	G	C	C	N
363	A	A	A	A	A	A	A	Y	A	R	A	N
364	A	A	A	A	A	A	A	A	A	N	C	A
365	C	C	C	C	C	C	T	Y	T	A	T	N
366	A	A	A	A	A	A	A	A	G	N	C	N
367	C	C	C	C	C	C	T	C	T	A	T	A
368	A	A	A	A	A	A	A	A	T	N	T	N
369	C	C	C	C	C	C	T	Y	A	N	C	N
370	T	T	T	T	T	T	T	T	C	N	T	N
371	T	T	T	T	T	T	T	T	C	N	T	N
372	C	C	C	C	C	C	C	C	A	N	T	N
373	A	A	A	A	A	A	A	A	A	A	A	A
374	A	A	A	A	A	A	A	A	A	N	A	A
375	G	G	G	G	G	G	T	N	T	N	T	N
376	T	T	T	T	T	T	G	N	G	N	G	N
377	A	A	A	A	A	A	T	T	A	N	T	N
378	T	T	T	T	T	T	C	Y	T	T/A	T	T/A
379	T	T	T	T	T	T	A	T	T	Y	T	Y
380	T	T	T	T	T	T	T	T/A	G	N	C	N
381	T	T	T	T	T	T	C	Y	A	Y	T	Y
382	T	T	T	T	T	T	A	T/A	T	T	C	N
383	A	A	A	A	A	A	T	A	G	N	C	N
384	C	C	C	C	C	C	G	C/G	A	R	A	N
385	A	A	A	A	A	A	A	A	G	R	A	N
386	C	C	C	C	C	C	A	A	C	N	T	N
387	A	A	A	A	A	A	A	A	A	N	A	A
388	C	C	C	C	C	C	A	A	C	N	A	N
389	A	A	A	A	A	A	A	A	A	N	C	N
390	G	G	G	G	G	G	C	Y	A	N	A	N
391	A	A	A	A	A	A	A	A	A	R	A	A
392	A	A	A	A	A	A	G	R	C	N	G	N
393	C	C	C	C	C	C	C	C	C	C	T	Y
394	T	T	T	T	T	T	A	T/A	A	T/A	C	N
395	T	T	T	T	T	T	A				G	
396												
397												
398	G	G	G	G	G	G	A	R	A	R		
399	A	A	A	A	A	A	T	N	T	N		
400	T	T	T	T	T	T	T	T	T	Y		
401	T	T	T	T	T	T	C	T	C	T		
402	T	T	T	T	T	T	T	T	T	Y		
403	C	C	C	C	C	C	C	T/A	G	N		
404	T	T	T	T	T	T	C	C	A	N		
405	T	T	T	T	T	T	C	C	A	N		
406	C	C	C	C	C	C	C	C	A	N		
407	T	T	T	T	T	T	A	R	A	N		
408	A	A	A	A	A	A	T	T	C	T		
409	T	T	T	T	T	T	G	A	T	R		
410	T	T	T	T	T	T	A	T	T	T		
411	T	T	T	T	T	T	T	T	T	AT		
412	G	G	G	G	G	G	T	T	T	T		
413	A	A	A	A	A	A	T	T	T	T		
414	T	T	T	T	T	T	T	T	T	T		
415	T	T	T	T	T	T	T	T	T	T		
416	T	T	T	T	T	T	T	T	T	T		
417	T	T	T	T	T	T	T	T	T	T		
418	T	T	T	T	T	T	T	T	T	T		
419	T	T	T	T	T	T	T	T	T	T		
420	T	T	T	T	T	T	T	T	T	T		
421	T	T	T	T	T	T	T	T	T	T		
422	T	T	T	T	T	T	T	T	T	T		
423	T	T	T	T	T	T	T	T	T	T		
424	T	T	T	T	T	T	T	T	T	T		
425	T	T	T	T	T	T	T	T	T	T		
426	T	T	T	T	T	T	T	T	T	T		
427	T	T	T	T	T	T	T	T	T	T		
428	T	T	T	T	T	T	T	T	T	T		
429	T	T	T	T	T	T	T	T	T	T		
430	T	T	T	T	T	T	T	T	T	T		
431	T	T	T	T	T	T	T	T	T	T		
432	T	T	T	T	T	T	T	T	T	T		
433	G	G	G	G	G	G	T	G	N	N		
434	A	A	A	A	A	A	A	N	N	N		
435	C	C	C	C	C	C	A	N	N	N		
436	T	T	T	T	T	T	A	N	N	N		
437	G	G	G	G	G	G	A	N	N	N		
438	A	A	A	A	A	A	A	N	N	N		
439	T	T	T	T	T	T	T	N	N	N		
440	T	T	T	T	T	T	T	N	N	N		
441	T	T	T	T	T	T	T	N	N	N		
442	T	T	T	T	T	T	T	N	N	N		
443	T	T	T	T	T	T	T	N	N	N		
444	T	T	T	T	T	T	T	N	N	N		
445	A	A	A	A	A	A	T	N	N	N		
446	C	C	C	C	C	C	A	N	N	N		
447							T	N	N	N		
448							G	N	N	N		
449							T	N	N	N		
450							G	N	N	N		
451							T	N	N	N		
452							T	N	N	N		
453							T	N	N	N		
454							T	N	N	N		
455							T	N	N	N		
456							T	N	N	N		
457							T	N	N	N		
458							T	N	N	N		
459							T	N	N	N		
460							T	N	N	N		
461							T	N	N	N		
462							T	N	N	N		
463							T	N	N	N		
464							T	N	N	N		
465							T	N	N	N		
466							T	N	N	N		
467							T	N	N	N		
468							T	N	N	N		
469							T	N	N	N		
470							T	N	N	N		
471							T	N	N	N		

FIG. 7.2 Cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
472	A	A	A	A	A	A	A	A		A	A	A
473	A	A	A	A	A	A	A	A		A	A	A
474	T	T	T	T	T	T	T	T		T	T	T
475	A	A	A	A	A	A	A	A		A	A	A
476	A	A	A	A	A	A	A	A		A	A	A
477	A	A	A	A	A	A	A	A		A	A	A
478	G	G	G	G	G	G	G	G		G	T	N
479	G	G	G	G	G	G	T	N		N	T	N
480	T	T	T	T	T	T	G	N		N	T	N
481	A	A	A	A	A	A	T	N		N	A	N
482	T	C	C	C	C	C	T	Y		N	A	N
483	A	T	T	T	T	T	T	T		Y	A	N
484	A	A	A	A	A	A	C	N		T	G	A/T
485	T	T	T	T	T	T	T	T		N	A	N
486	C	C	C	C	C	C	G	N		N	A	N
487	G	G	G	G	G	G	A	R		R	A	R
488	T	T	T	T	T	T	T	T		T	A	T/A
489	T	T	T	T	T	T	G	N		N	A	N
490	A	A	A	A	A	A	A	N		N	A	N
491	T	T	T	T	T	T	A	R		N	A	N
492	G	G	G	G	G	G	T	N		R	A	N
493	T	A	A	A	A	N	A	N		N	A	A
494	A	A	A	A	A	A	A	A		A	A	A
495	A	A	A	A	A	A	A	A		A	A	A
496	A	A	A	A	A	A	A	A		A	A	A
497	A	A	A	A	A	A	A	A		A	A	A
498	A	A	A	A	A	A	A	A		A	A	A
499	A	A	A	A	A	A	A	A		A	A	A
500	A	A	A	A	A	A	A	A		A	A	A
501	A	A	A	A	A	A	A	A		A	A	A
502	A	A	A	A	A	A	A	A		A	A	A
503	A	A	A	A	A	A	A	A		A	A	A
504	A	A	A	A	A	A	A	A		A	A	A
505	A	A	A	A	A	A	A	A		A	A	A
506	A	A	A	A	A	A	A	A		A	A	A
507	A	A	A	A	A	A	A	A		A	A	A
508	A	A	A	A	A	A	A	A		A	A	A
509	A	A	A	A	A	A	A	A		A	A	A
510	A	A	A	A	A	A	A	A		A	A	A
511	A	A	A	A	A	A	A	A		A	A	A
512	A	A	A	A	A	A	A	A		A	A	A

FIG. 7.2 Cont.

09876348-060701

1020200104132050

Position	Tm 12.64-2.2	Tm 12.64-2.3	Tm 12.64-3.4	Tm 12.64-3.9	Tm 12.64-7.5	Consensus Tm 12.84	Tm 13.17	Consensus to Tm 13.17	Tm P.81	Tm P.82	Consensus to B1B2	Tm AFP-3	Consensus to AFP-3	GENERAL CONSENSUS	SUBSTITUTIONS - most to least common
1	M	M	M	M	M	M	M	M	M	M	M	M	M	K	
2	K	K	K	K	K	K	K	K	K	K	K	K	K	L	
3	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
4	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
5	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
6	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
7	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
8	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
9	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
10	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
11	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
12	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
13	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
14	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
15	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
16	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
17	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
18	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
19	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
20	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
21	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
22	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
23	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
24	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
25	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
26	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
27	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
28	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
29	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
30	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
31	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
32	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
33	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
34	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
35	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
36	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
37	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
38	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
39	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
40	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
41	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
42	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
43	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
44	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
45	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
46	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
47	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
48	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
49	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
50	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
51	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
52	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
53	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
54	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
55	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
56	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
57	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
58	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
59	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
60	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
61	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
62	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
63	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
64	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
65	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
66	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
67	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
68	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
69	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
70	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
71	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
72	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
73	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
74	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
75	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
76	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
77	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
78	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
79	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
80	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
81	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
82	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
83	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
84	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
85	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
86	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
87	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
88	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
89	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
90	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
91	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
92	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
93	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
94	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
95	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
96	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
97	L	L	L	L	L	L	L	L	L	L	L	L	L	L	

FIG. 7.3

Position	Tm 12.84-12.2	Tm 12.84-12.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Concomitant	Tm P.81	Tm P.82	Concomitant	Tm AFR-3	Concomitant	GENERAL	SUBSTITUTIONS - read to least common
96	V	D	D	D	D	ALPHALP	E	E	ALPHALP	D	ALPHALP	D	E
97	K	K	K	K	K	K	K	K	K	D	ALPHALP	K	D
98	I	V	I	I	I	I	V	V	I	V	HY, BAS/ACD	V	L
99	V	V	V	V	V	V	V	V	V	V	ACD	V	I
100	O	O	O	O	O	ALP	E	E	ALP	A	HY, BAS/ACD	O	E
101	K	K	K	K	K	ALP	K	K	ALP	V	ACD	V	M
102	K	K	K	K	K	ALP	K	K	ALP	A	ACD	V	A
103	V	V	V	V	V	ALP	V	V	ALP	V	ALPHALP	V	
104	V	V	V	V	V	ALP	V	V	ALP	V	ALPHALP	V	
105	V	V	V	V	V	ALP	V	V	ALP	V	ALPHALP	V	
106	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
107	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
108	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
109	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
110	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
111	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
112	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
113	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
114	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
115	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
116	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
117	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
118	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
119	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
120	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
121	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
122	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
123	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
124	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
125	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
126	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
127	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
128	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
129	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
130	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
131	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
132	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
133	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
134	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
135	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
136	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	
137	K	K	K	K	K	ALP	V	V	ALP	V	HY, ACD/BAS	V	

FIG. 7.3 Cont.

09876348.060701

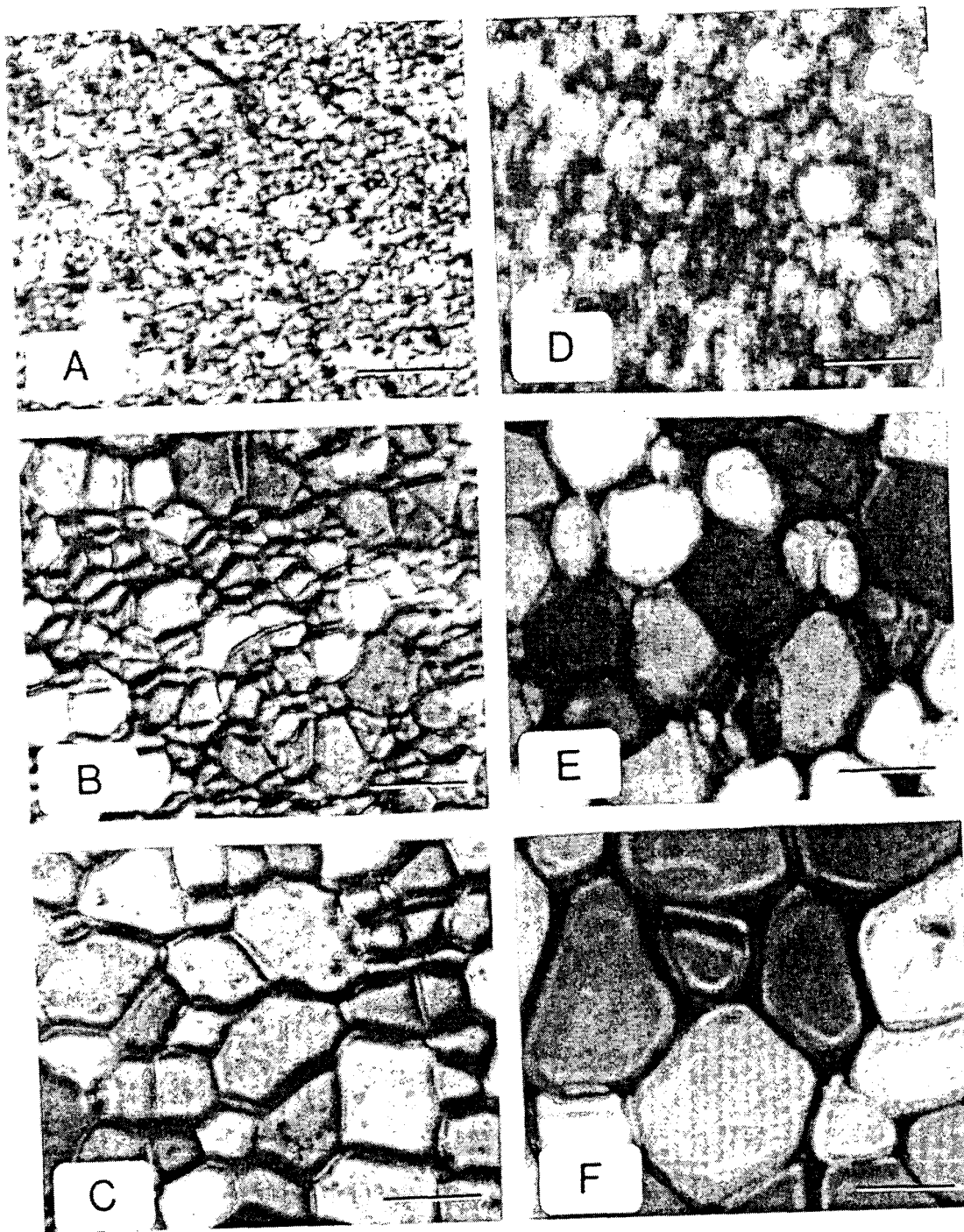


FIG. 8.0

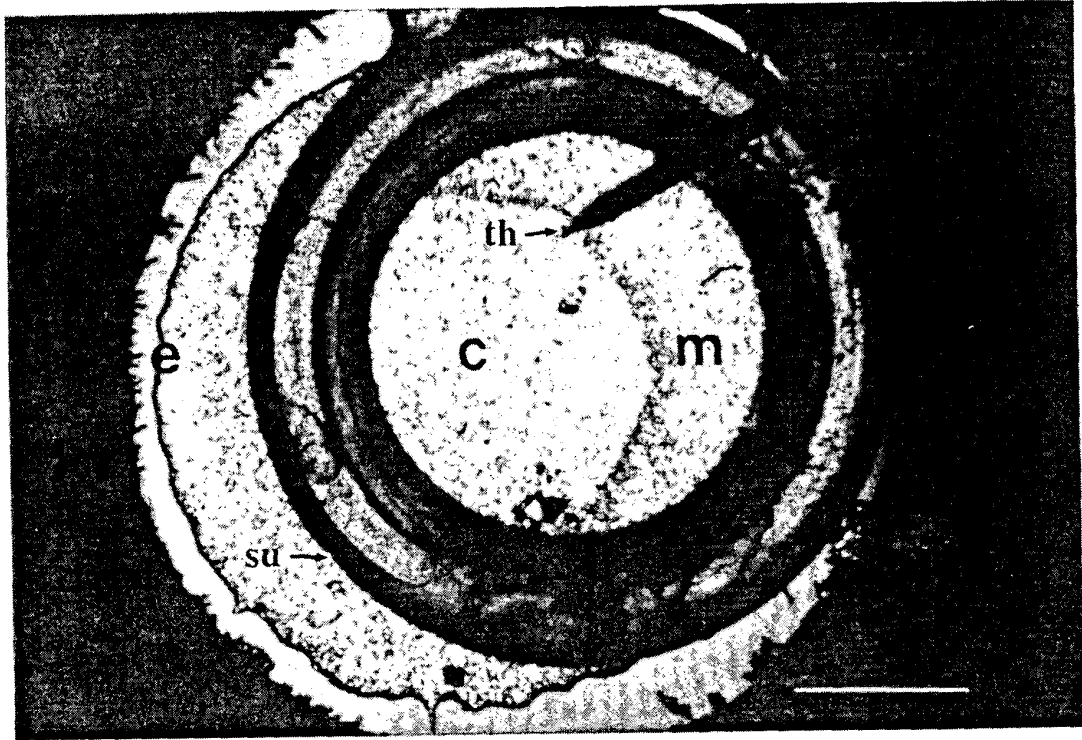


FIG. 8.1a

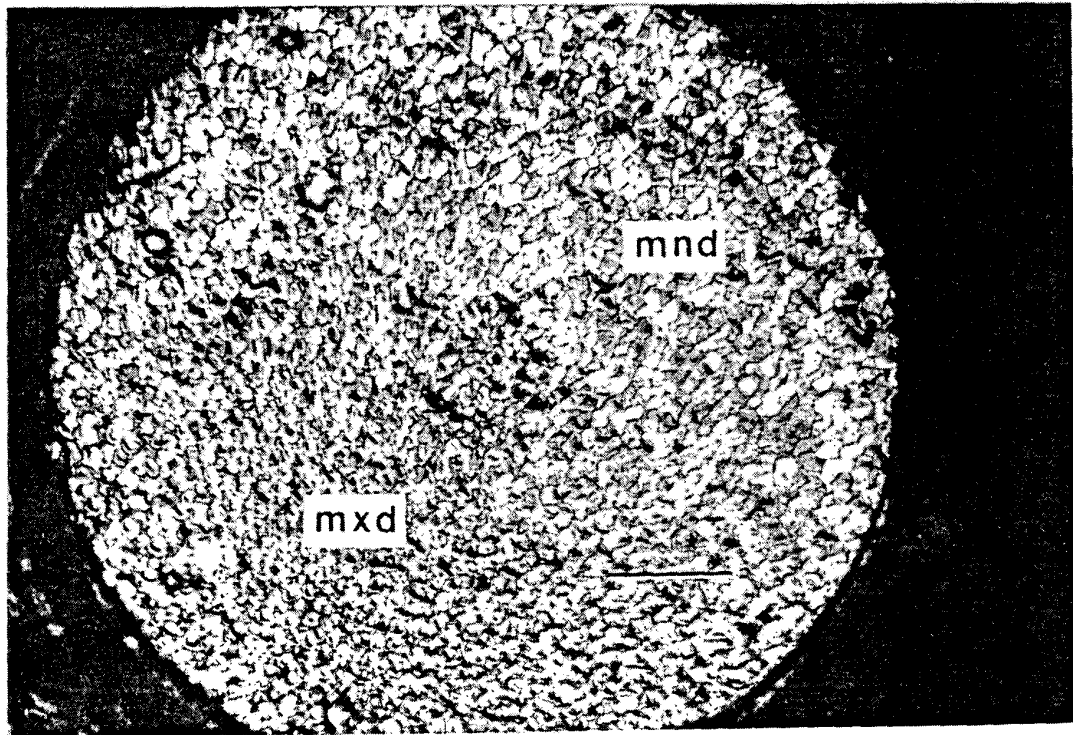
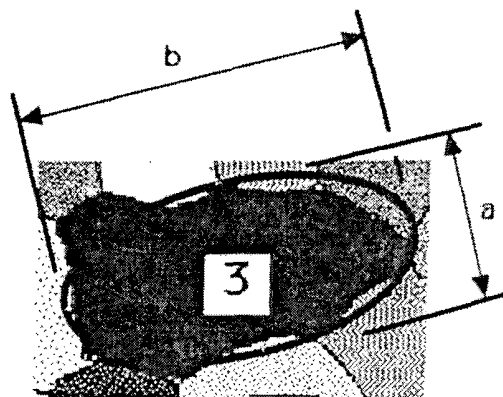
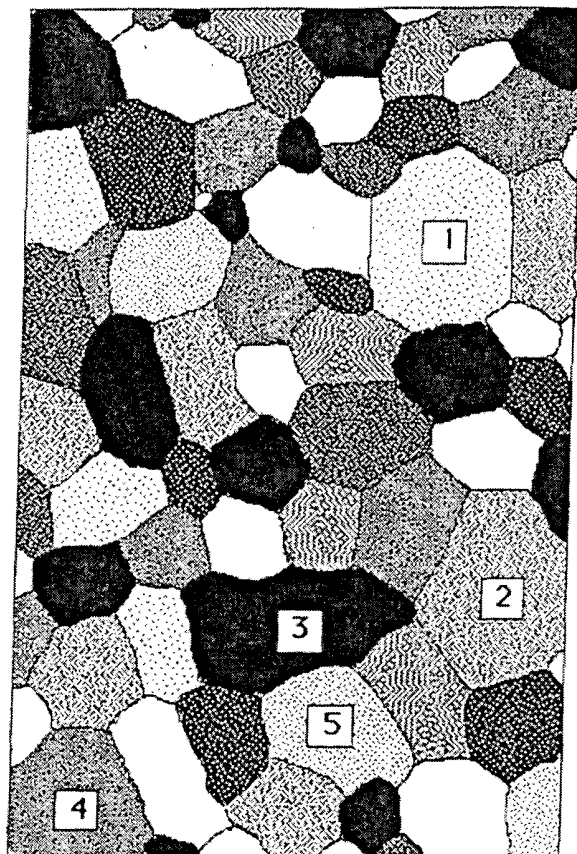


FIG. 8.1b



grain area = $0.25\pi ab$

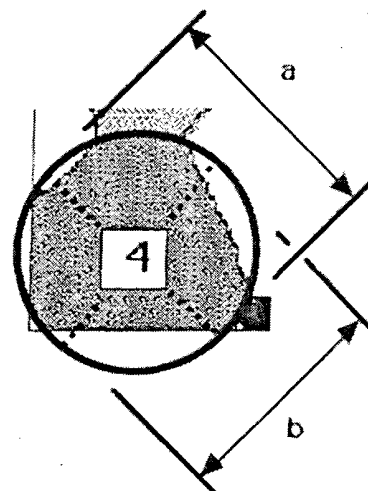


FIG. 8.2

09876348.060701
T07090" 84E9Z860

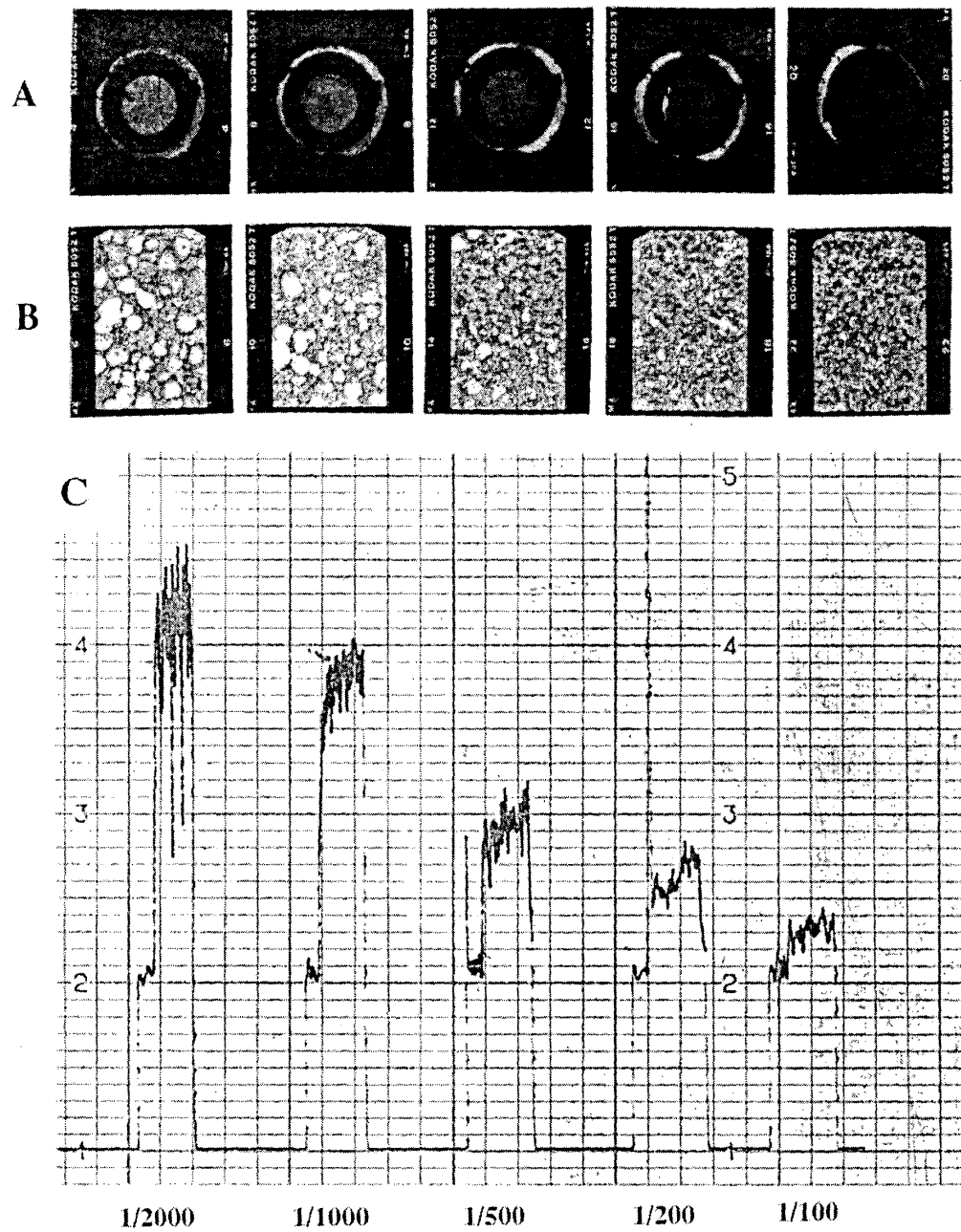


FIG. 8.3

A bar chart comparing the mean largest grain size (in mm²) across three categories: center, mid-sample, and edge. The y-axis represents the mean largest grain size, ranging from 0 to 0.015. The x-axis represents the category. For each category, there are two bars: a dotted bar and a shaded bar. Error bars are shown for each bar.

Category	Dotted Bar (Mean)	Shaded Bar (Mean)
center	~0.0015	~0.0108
mid-sample	~0.0015	~0.0100
edge	~0.0013	~0.0118

FIG. 8.4a

09876348.060701

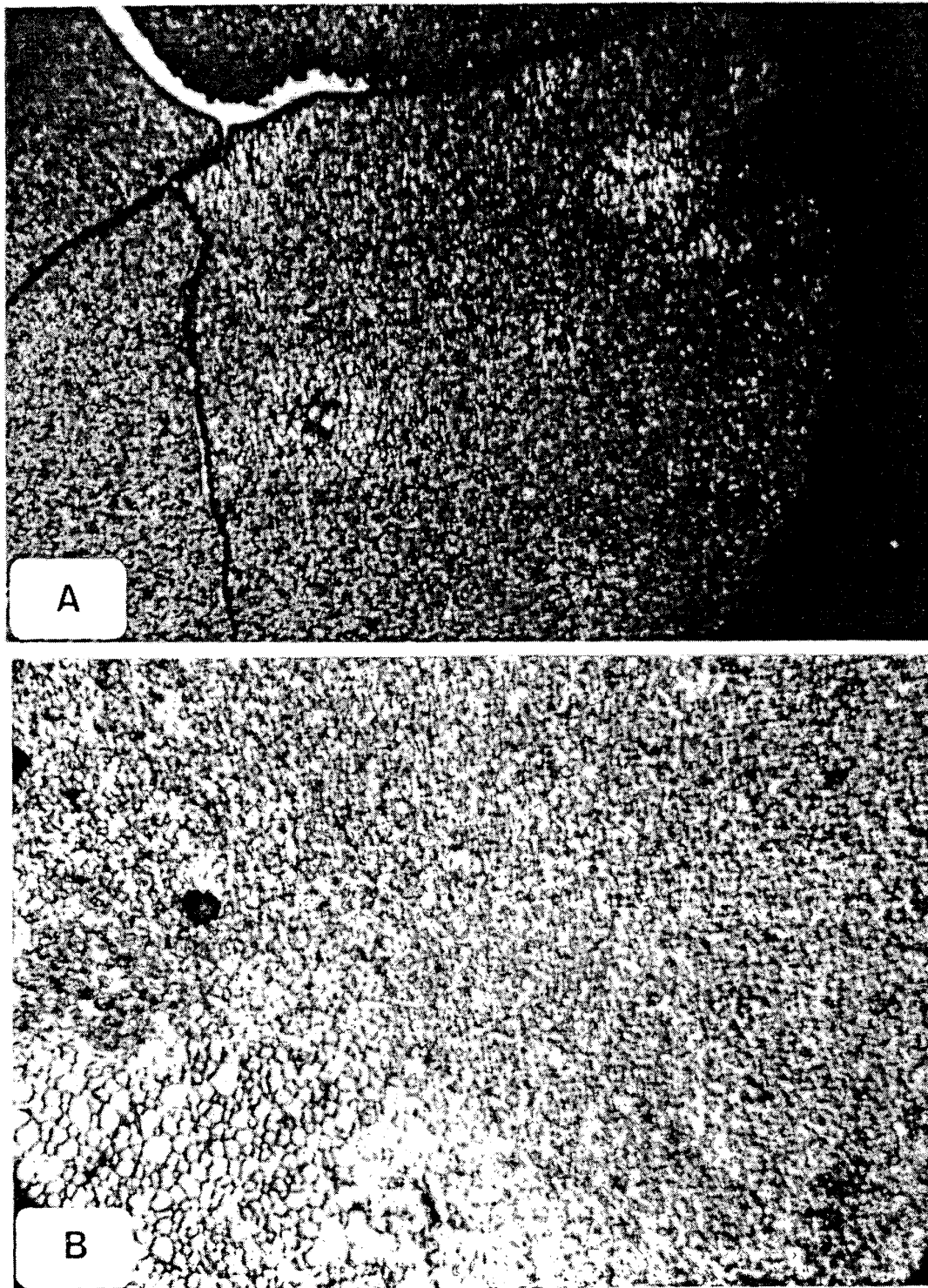


FIG. 8.4b

10/090" 84E9/860

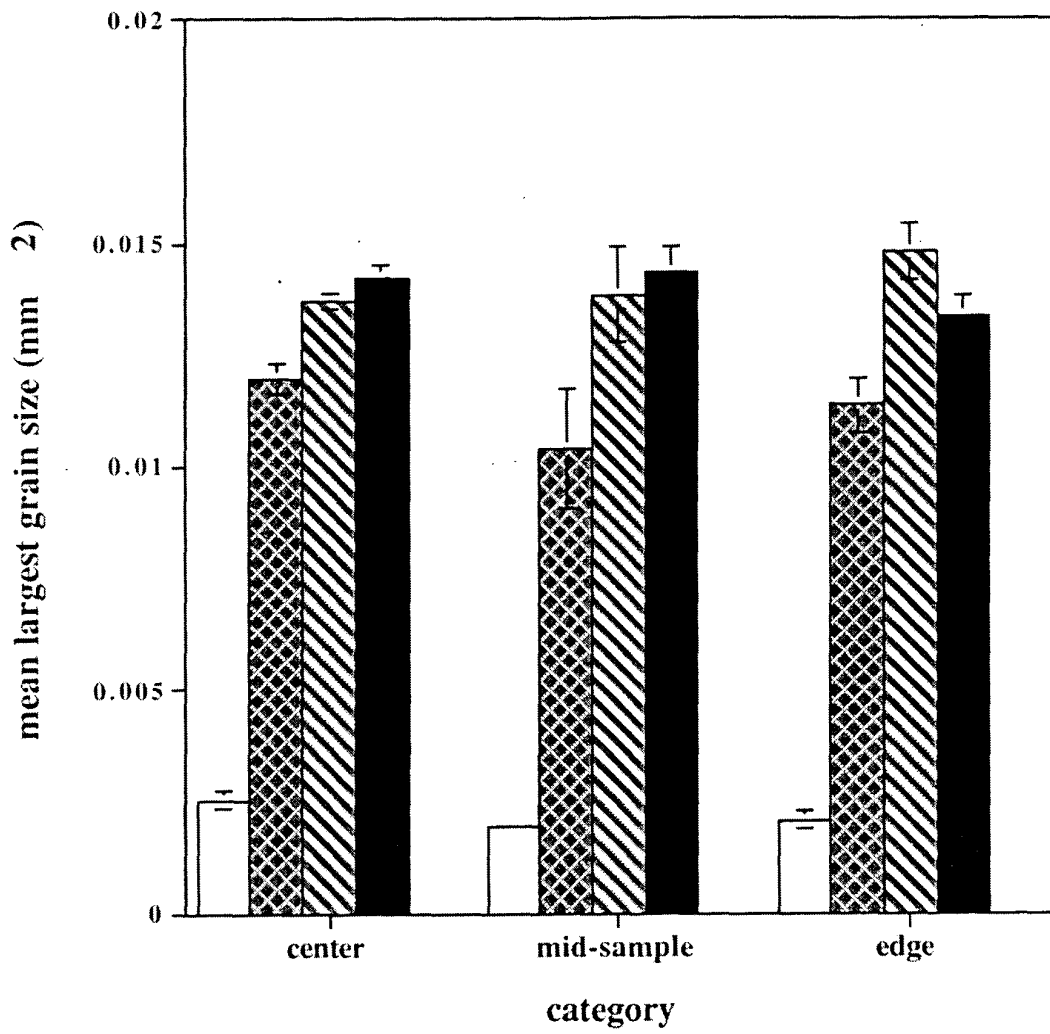


FIG. 8.5a

09676348-060704

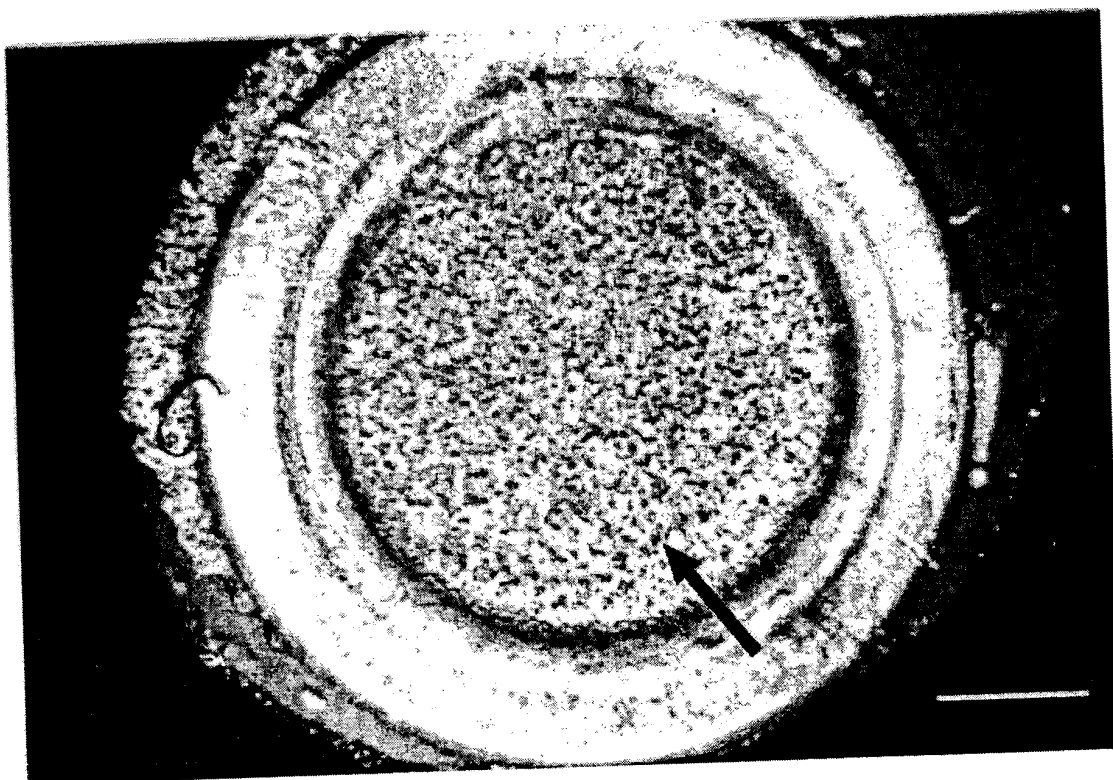


FIG. 8.5b

09876348-060701

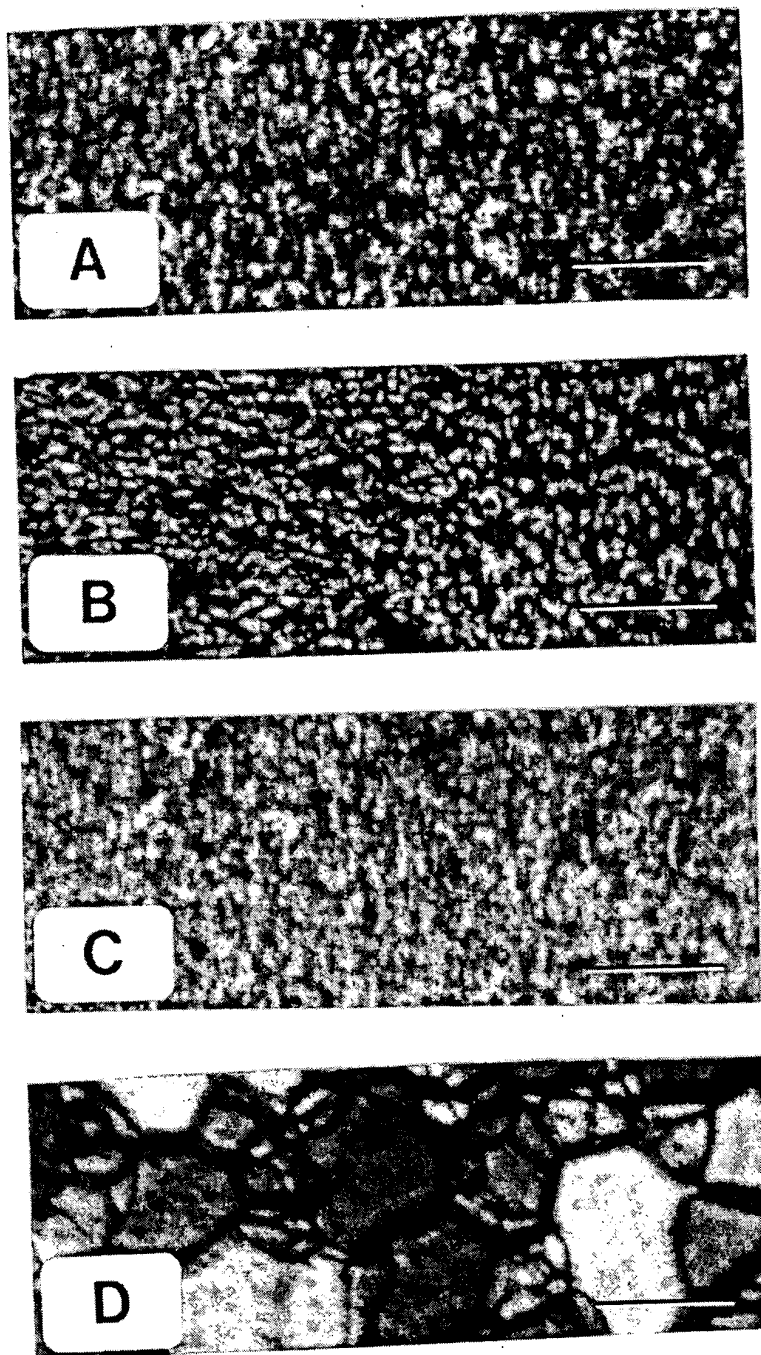


FIG. 8.6

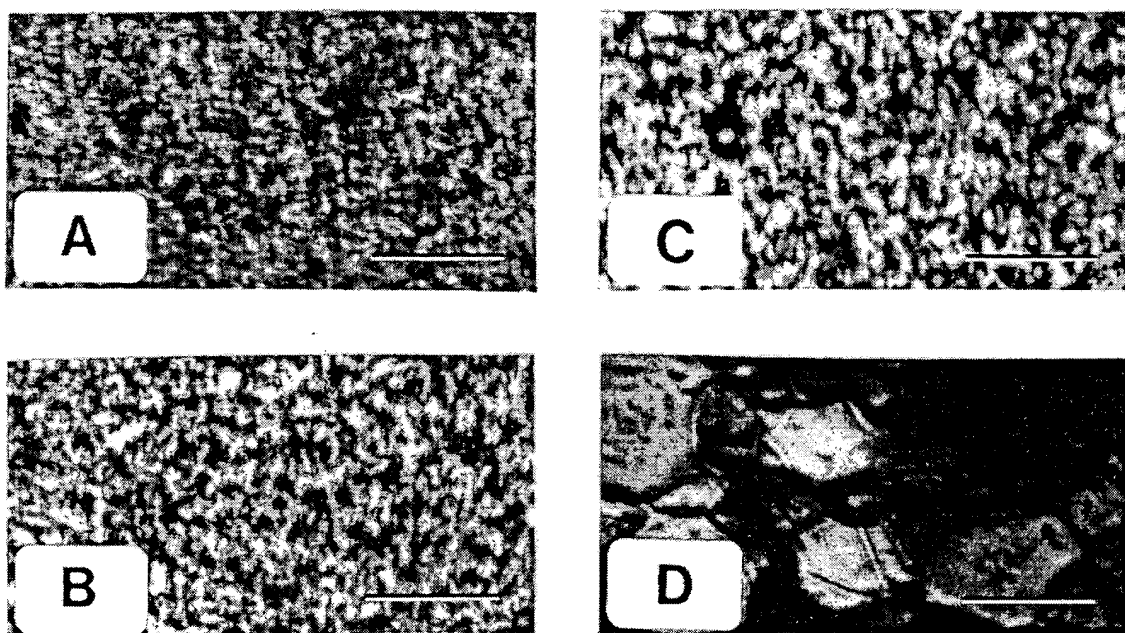


FIG. 8.7

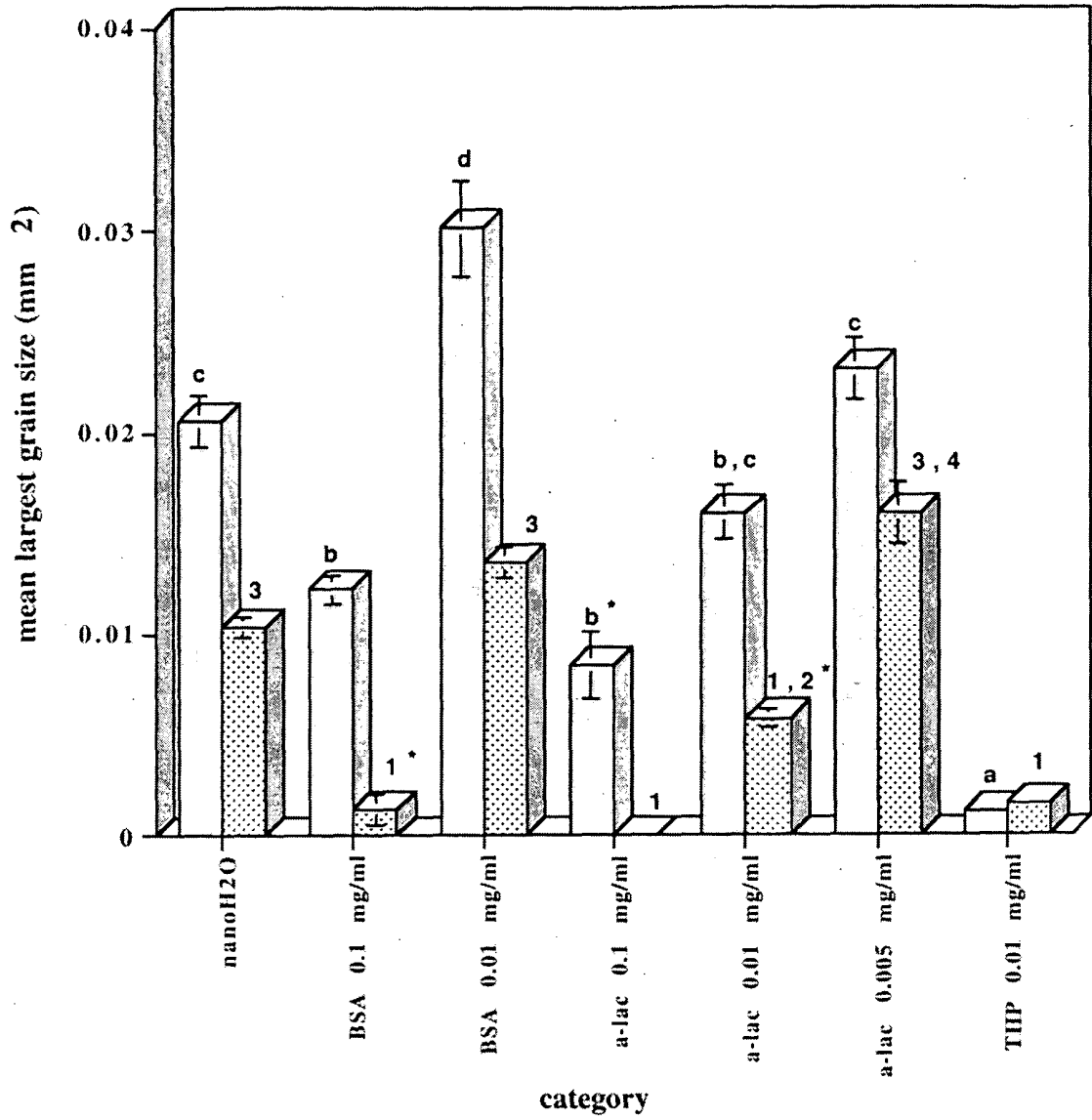


FIG. 8.8

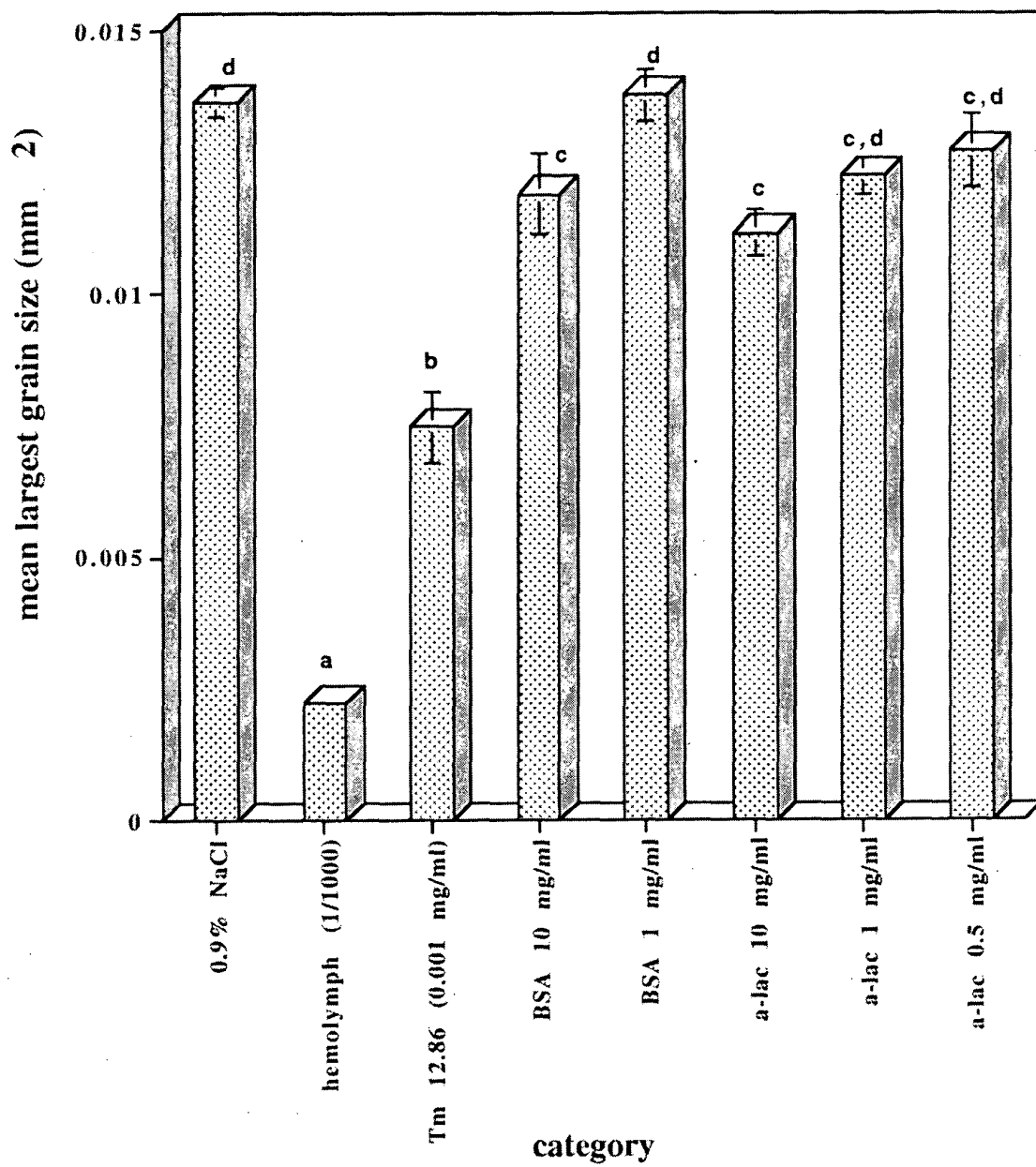


FIG. 8.9

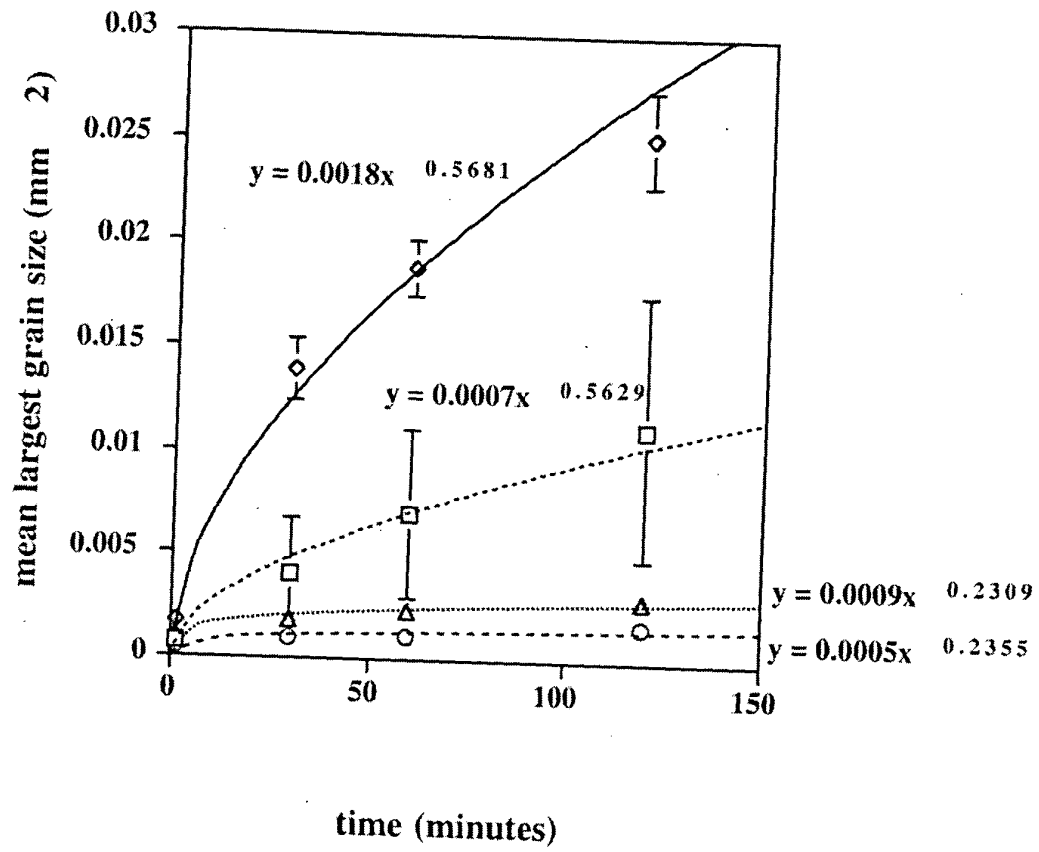


FIG. 8.10

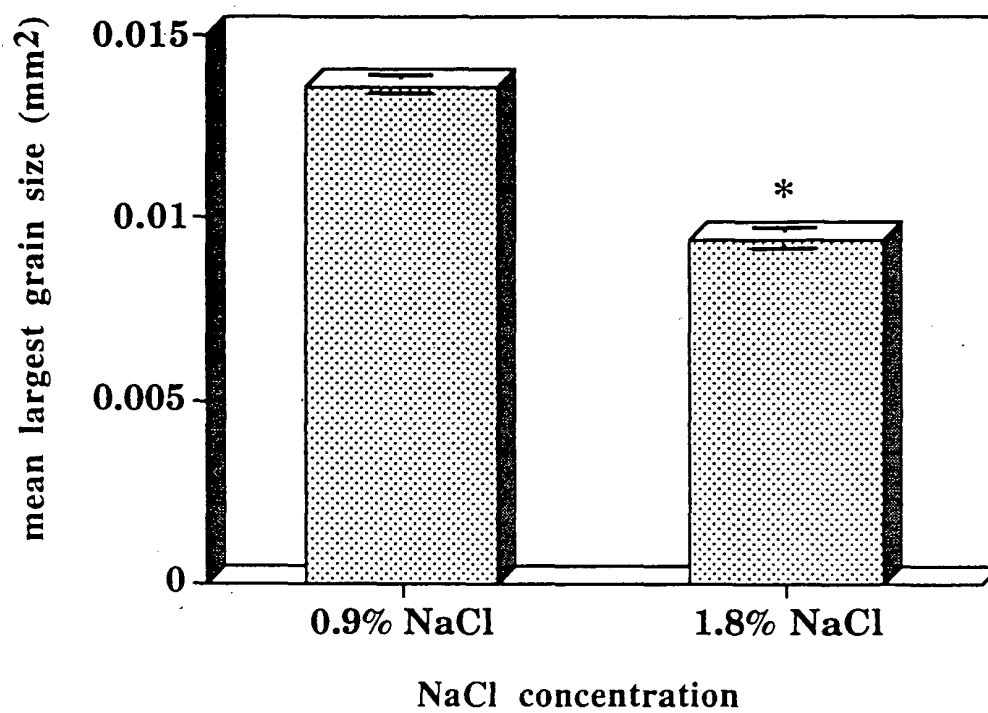


FIG. 8.11

09876348.060701

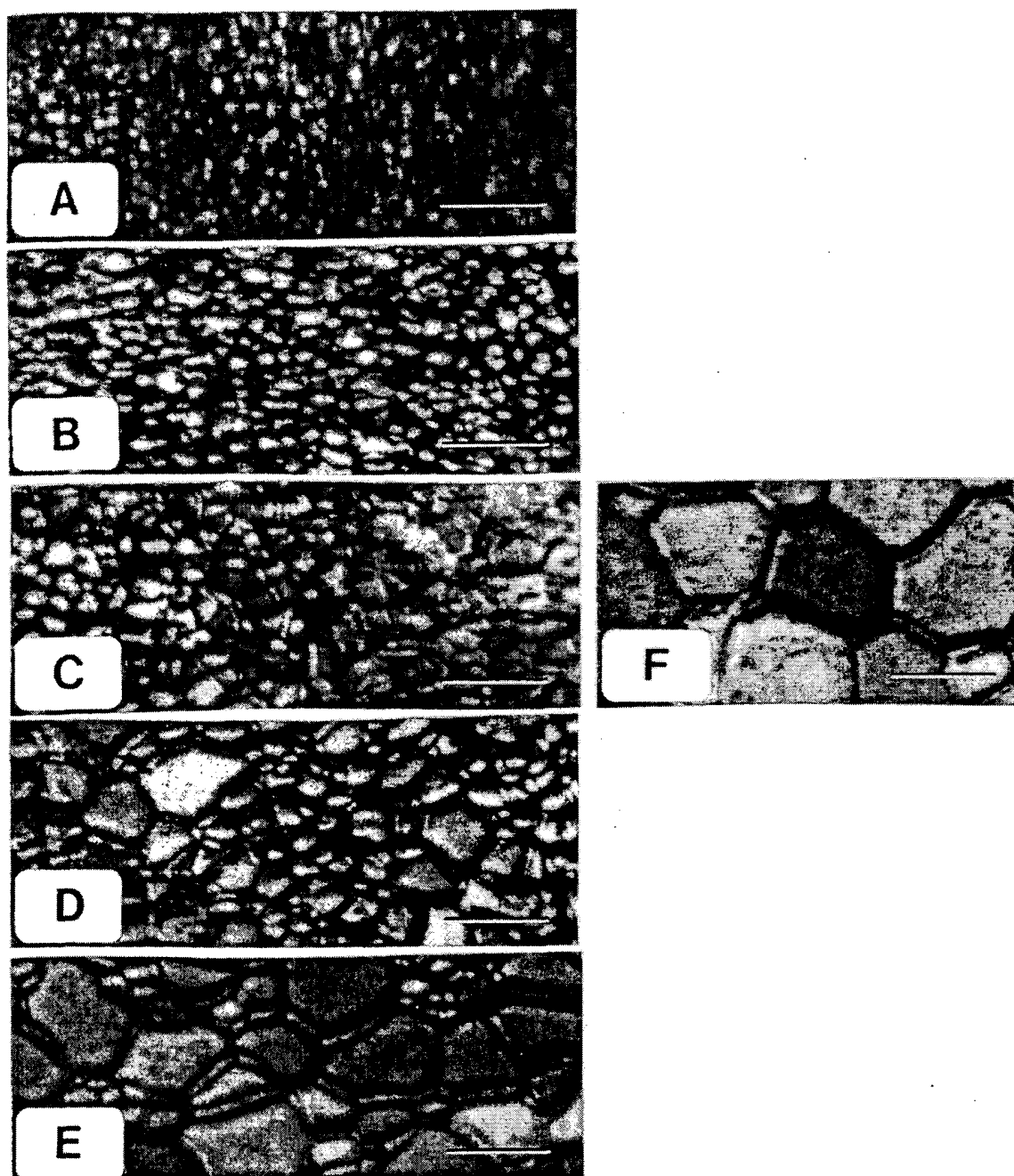


FIG. 8.12

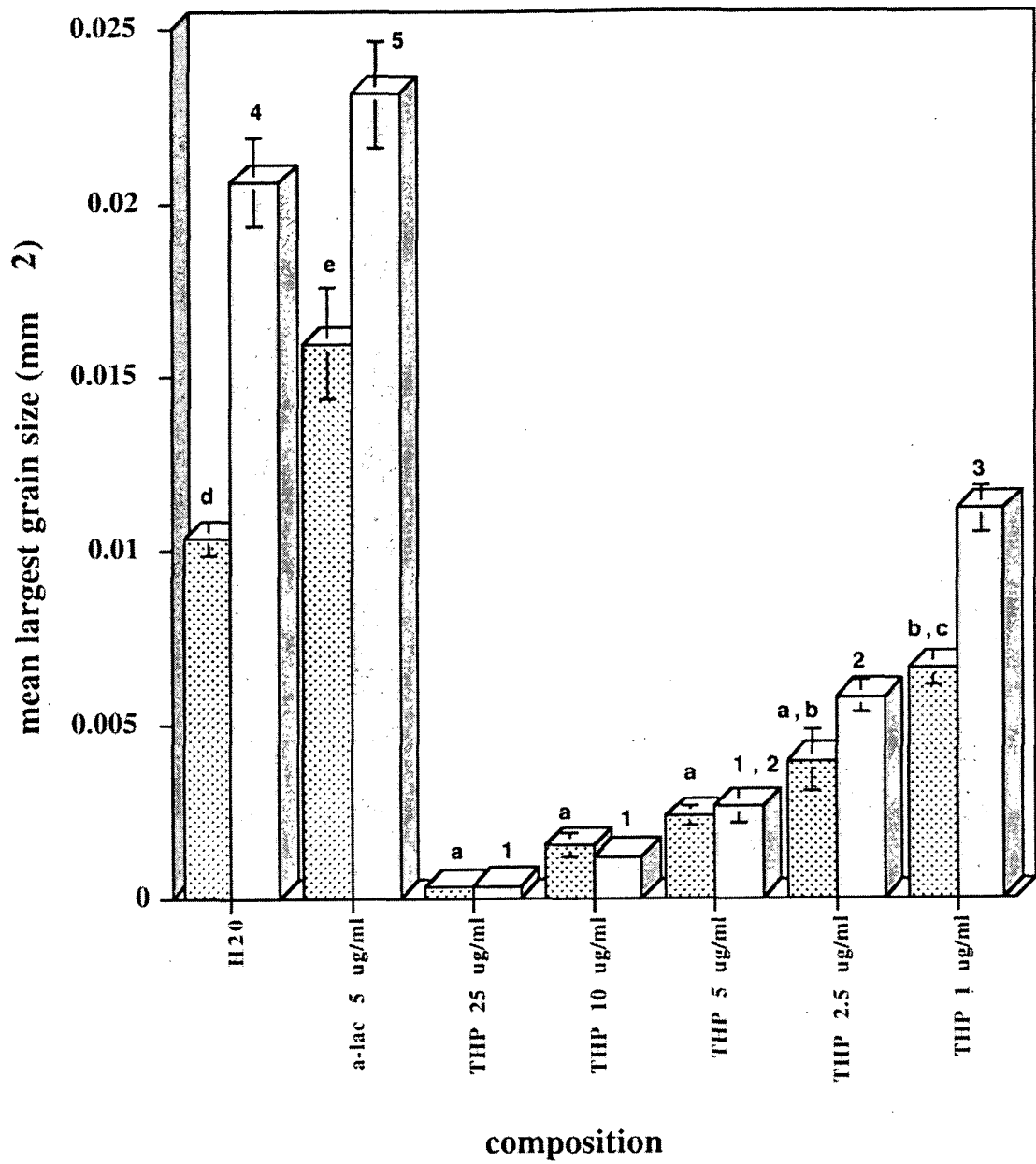


FIG. 8.13

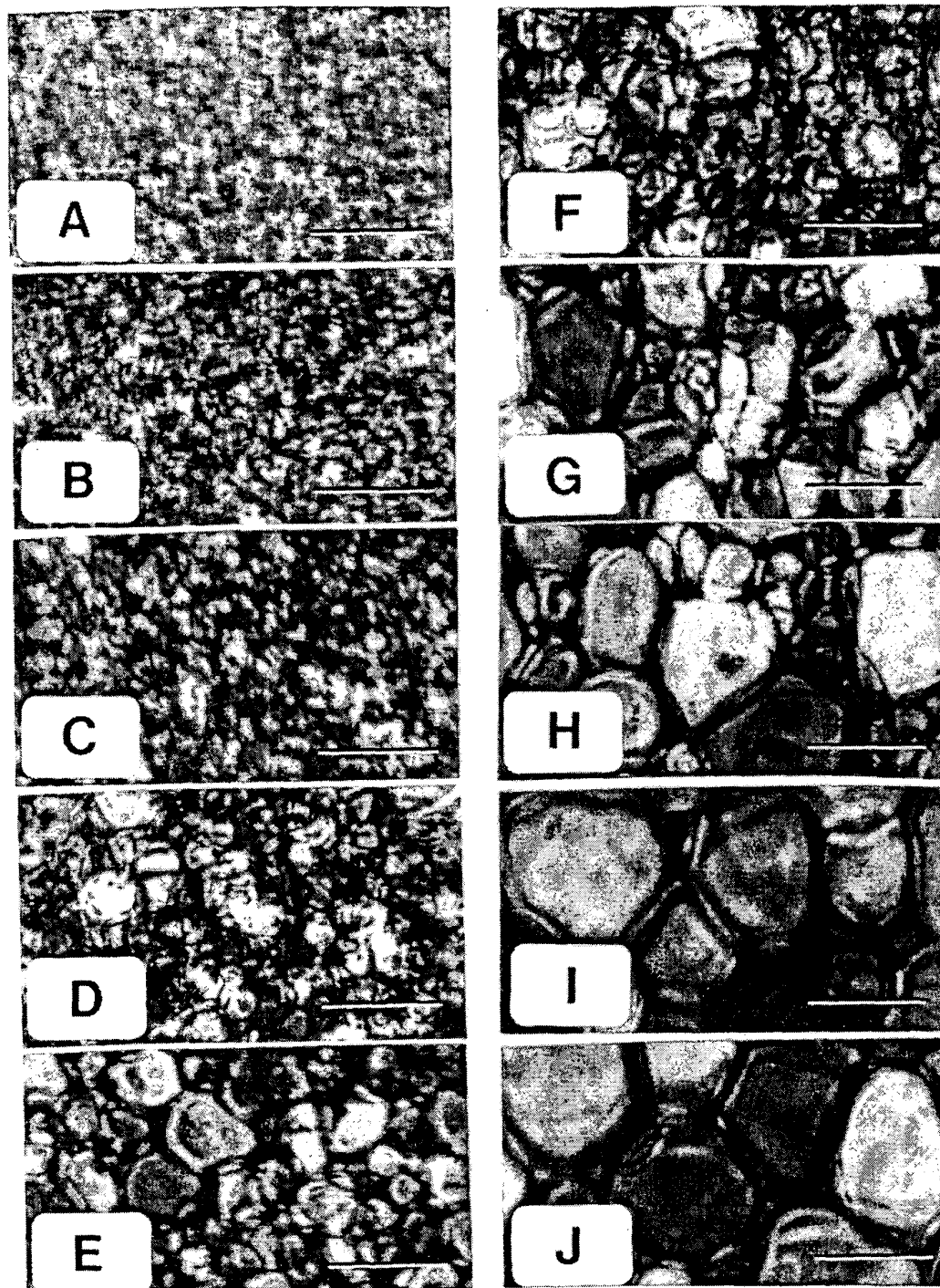


FIG. 8.14

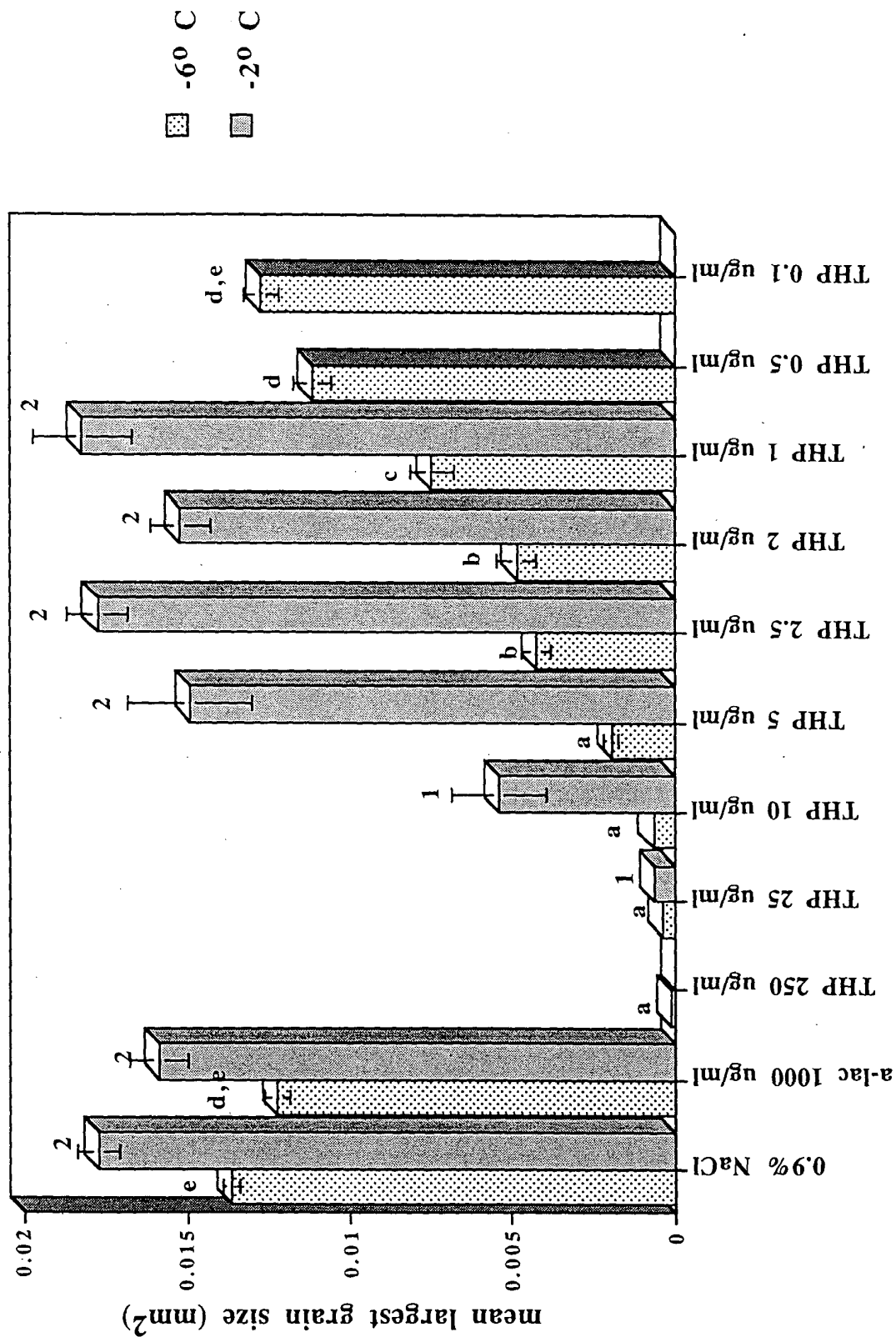


FIG. 8.15

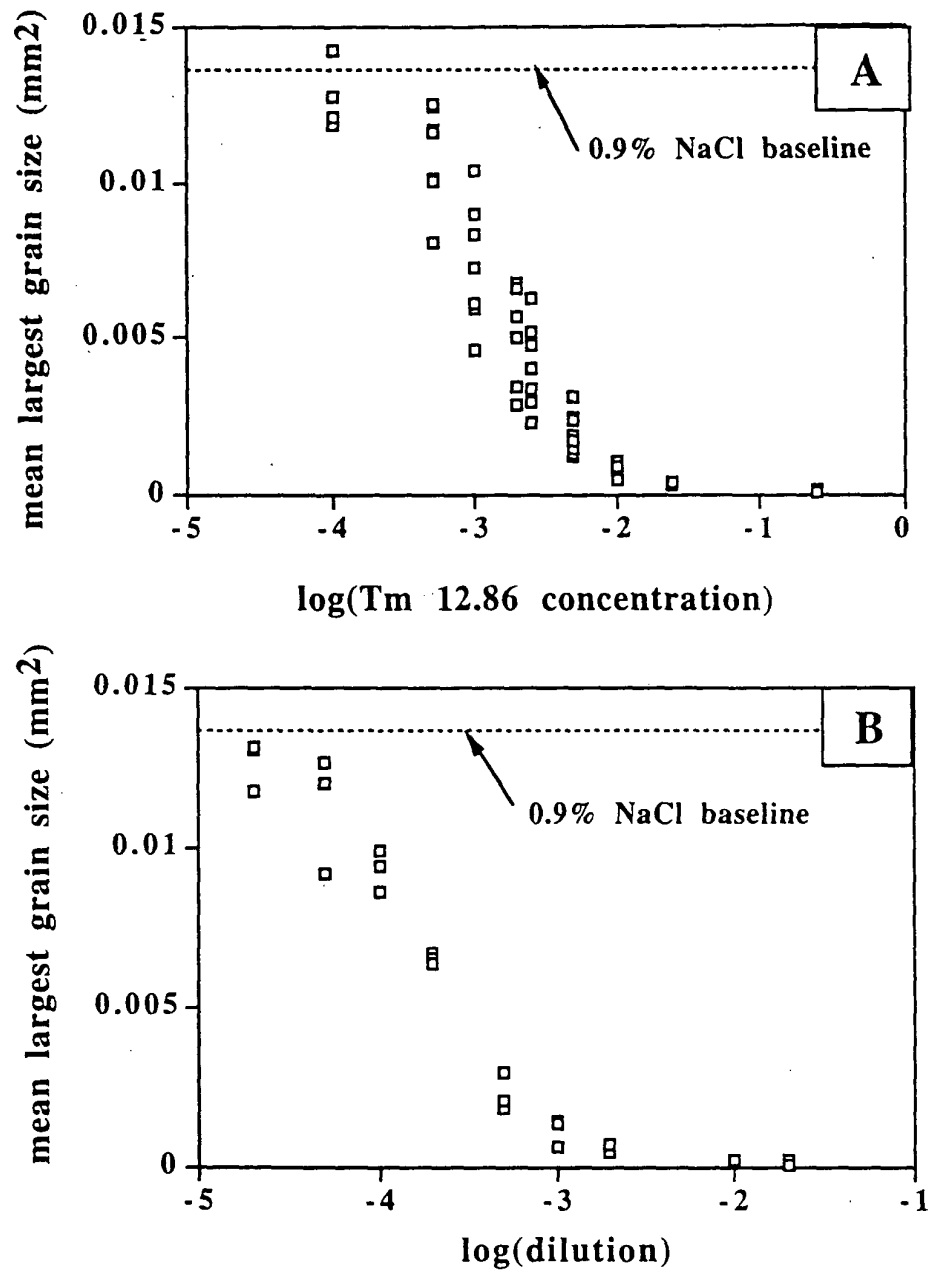


FIG. 8.16

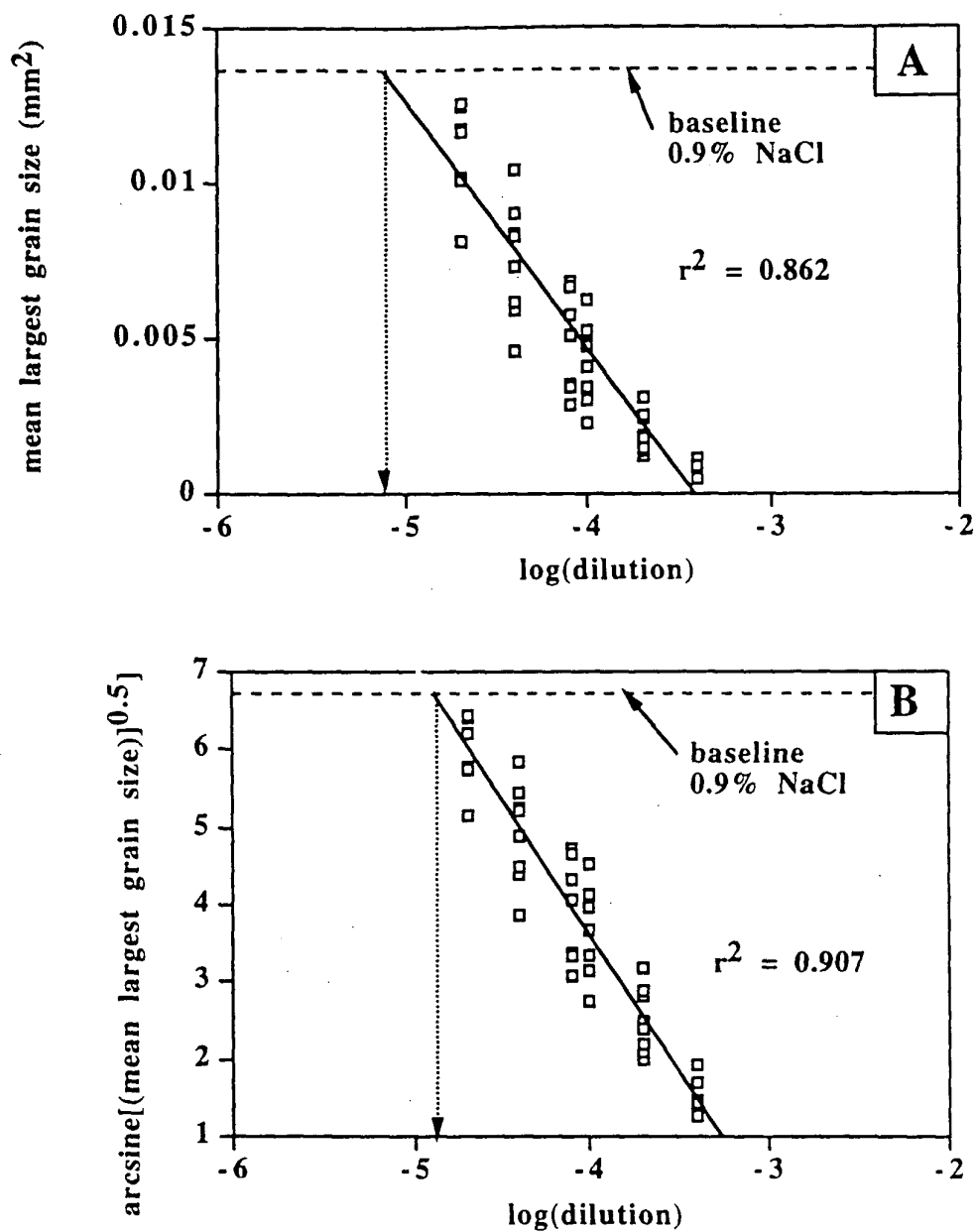


FIG. 8.17

09876348-060701
FO2090-84E92860

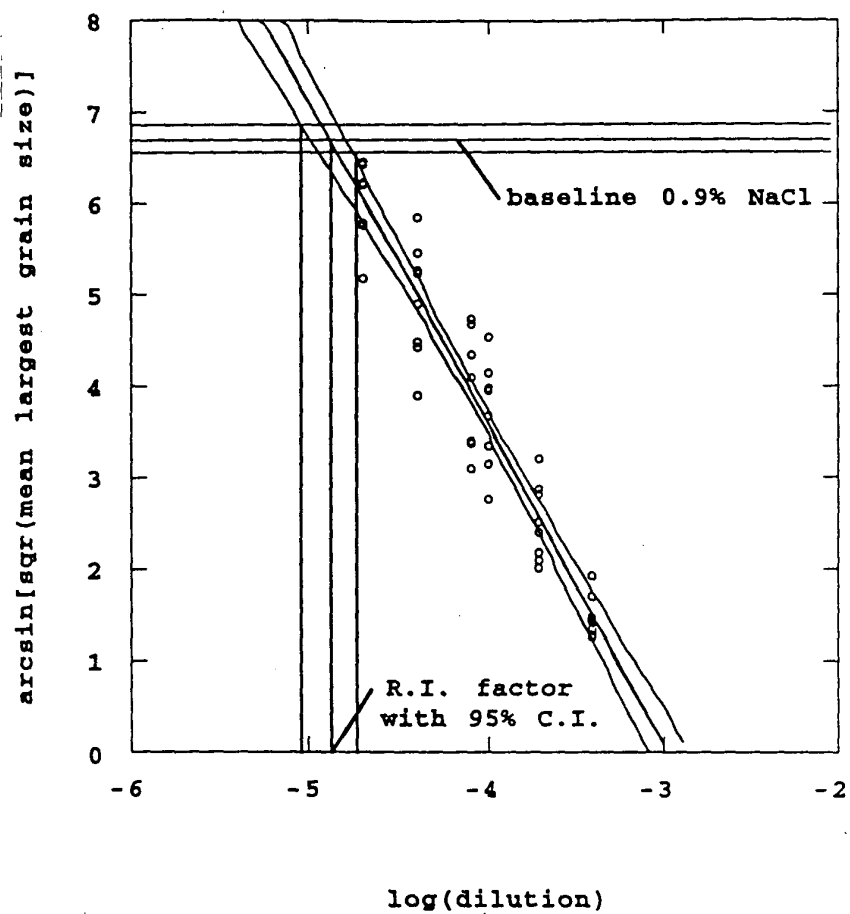


FIG. 8.18

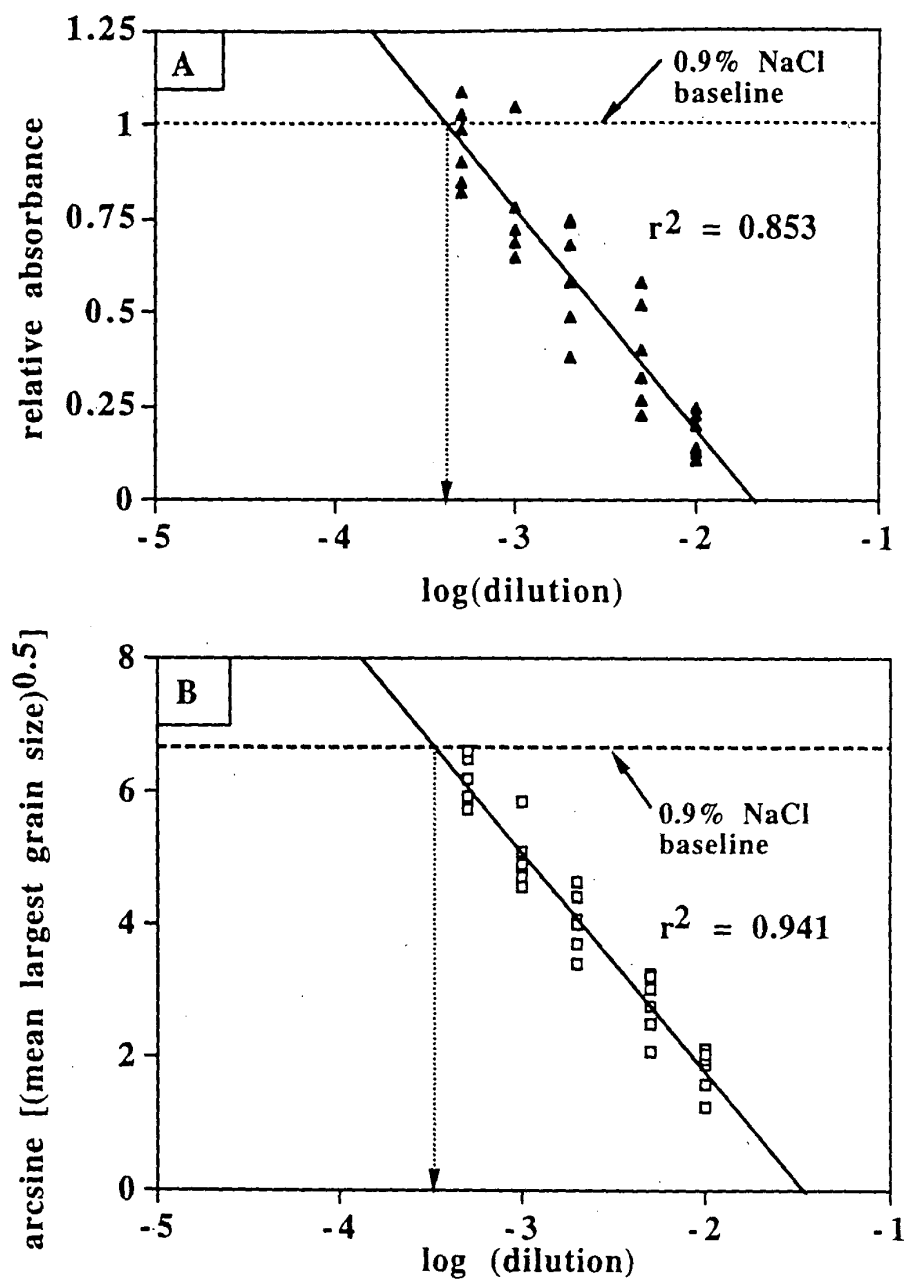


FIG. 8.19

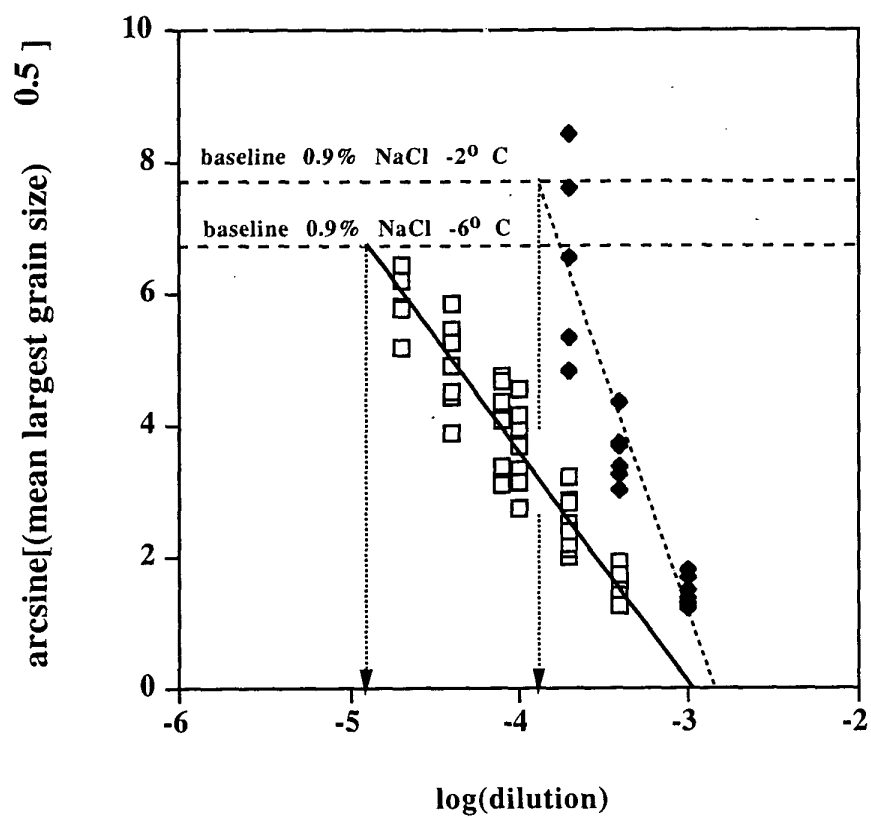


FIG. 8.20

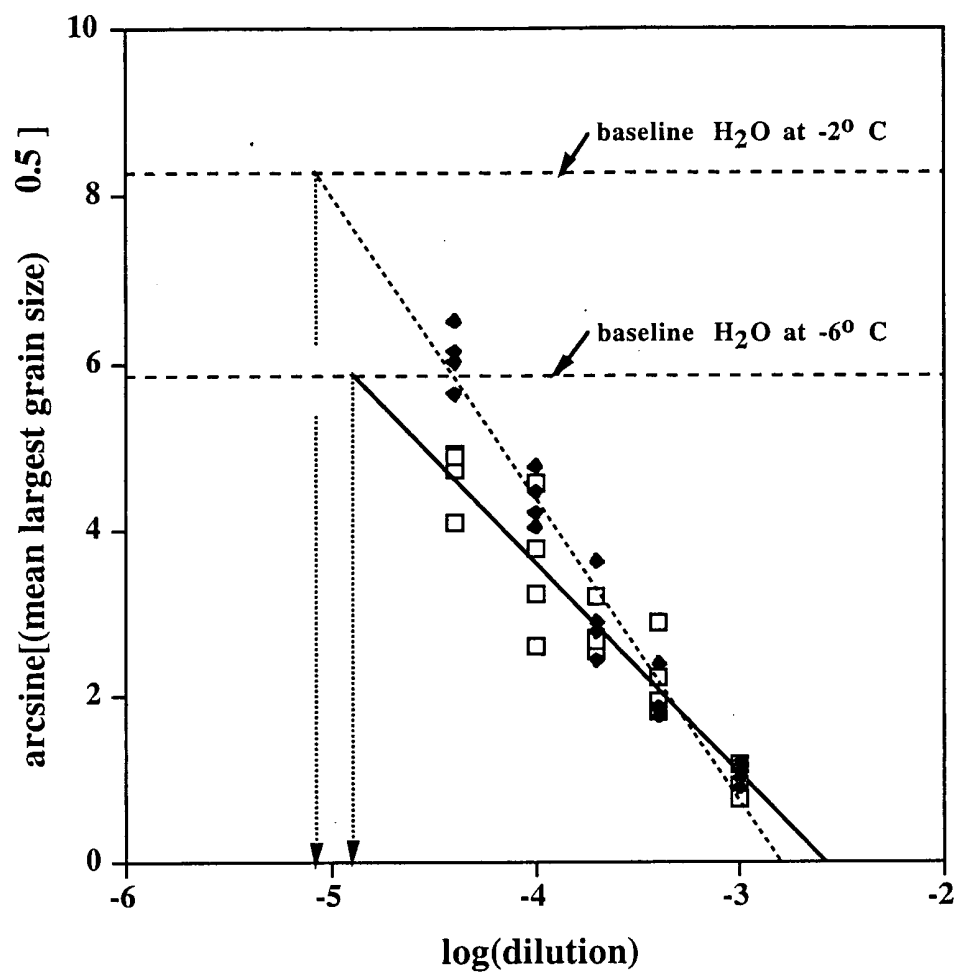


FIG. 8.21

104090" 84E94860

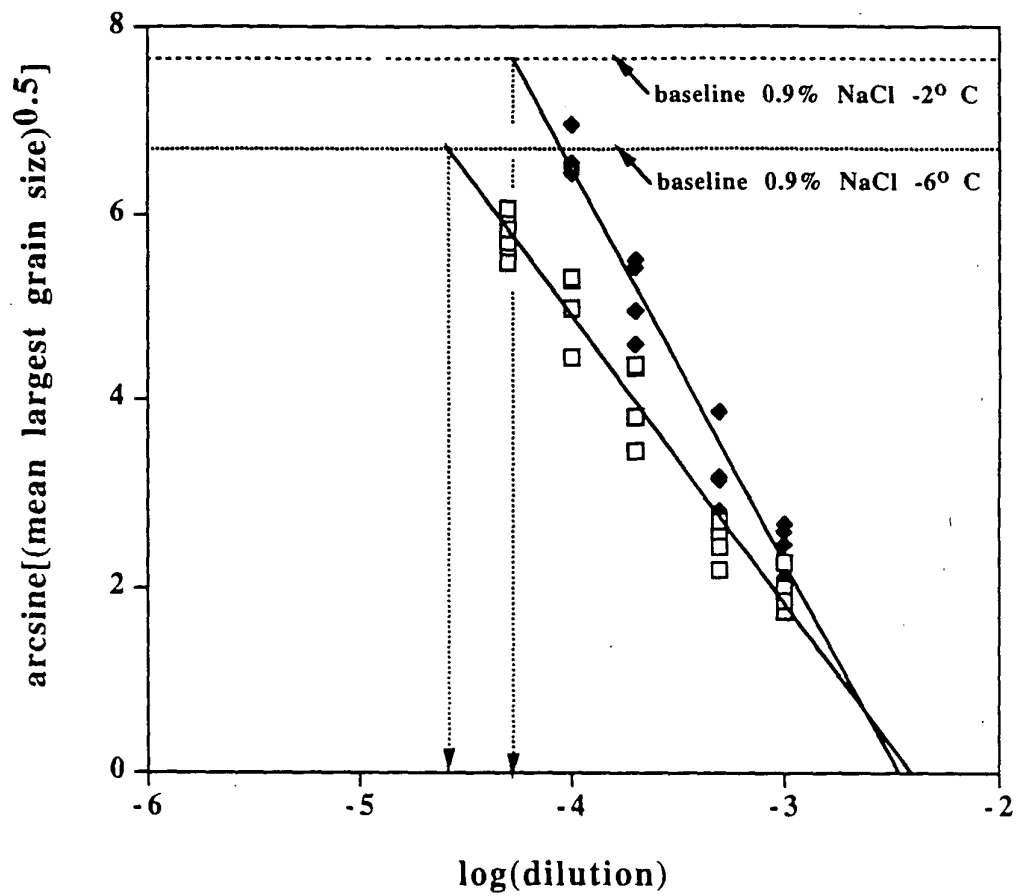


FIG. 8.22

FIG. 8.23

704090-07E92860

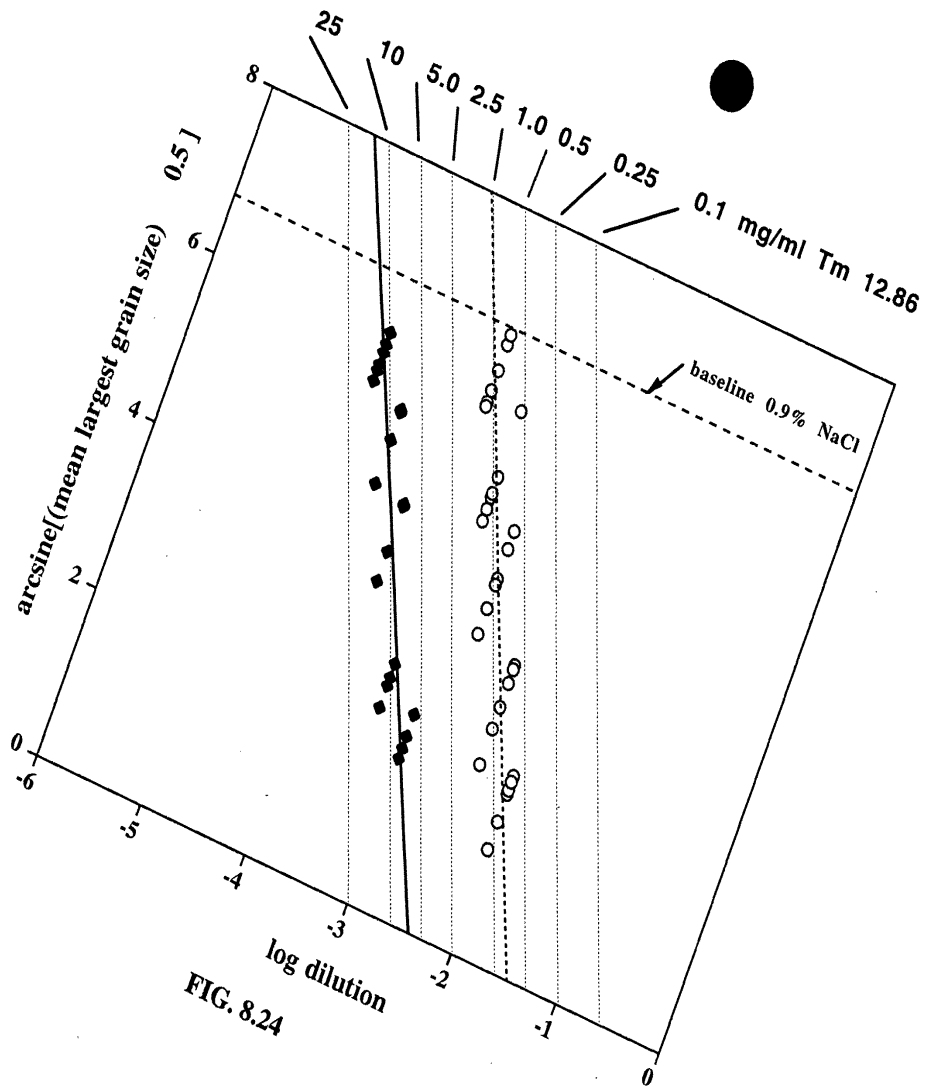


FIG. 8.24

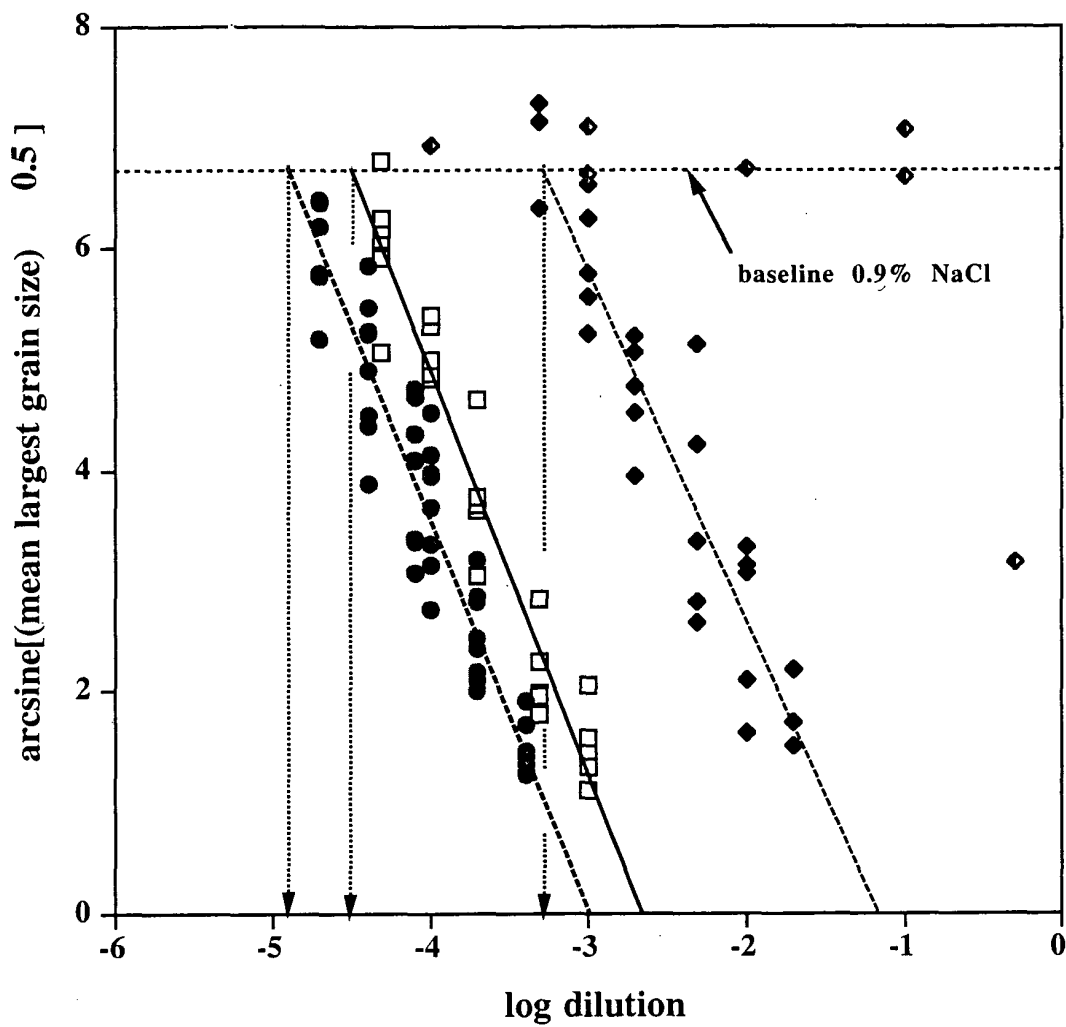


FIG. 8.25

008644-87E92860

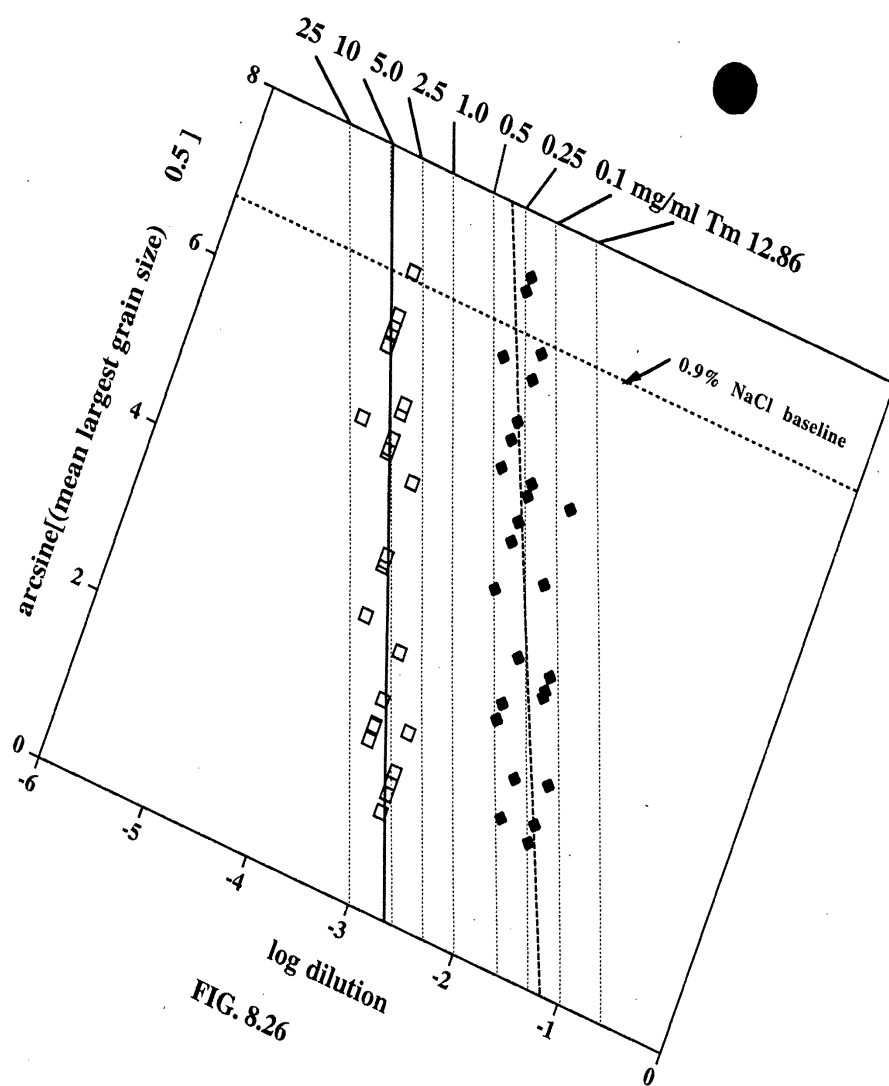


FIG. 8.26

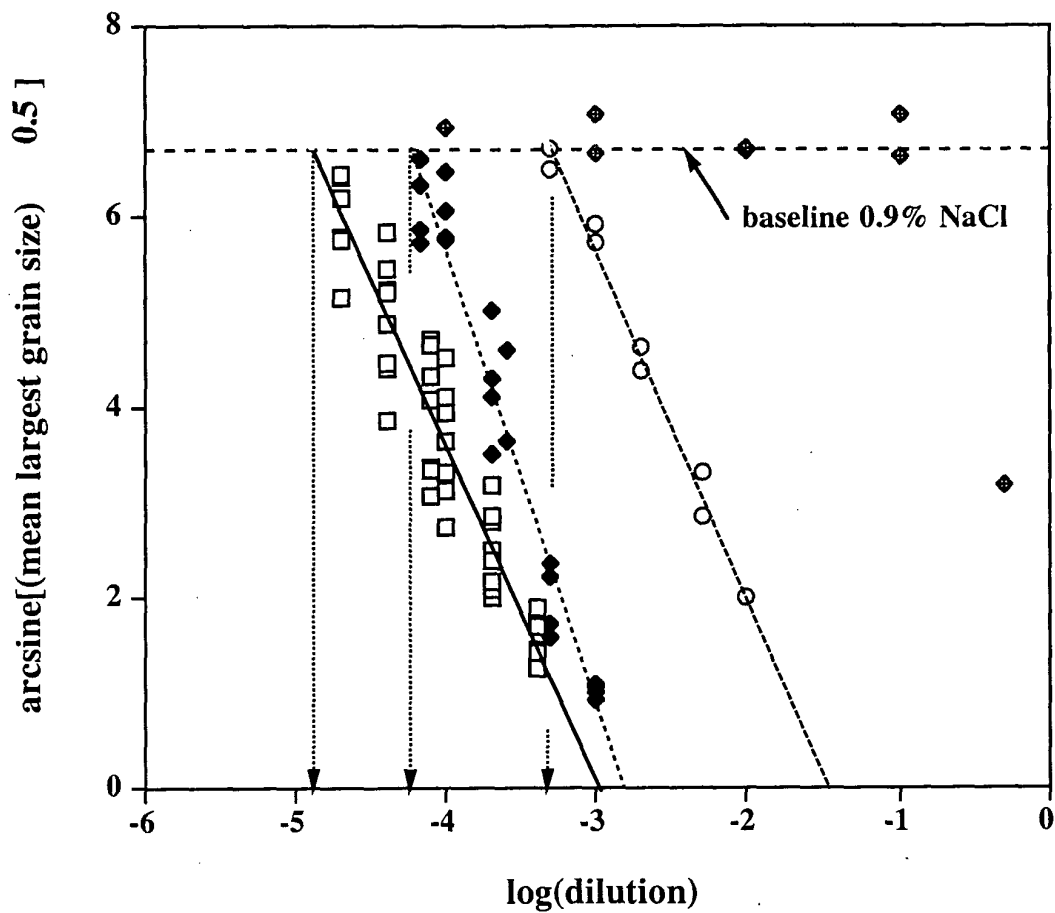


FIG. 8.27

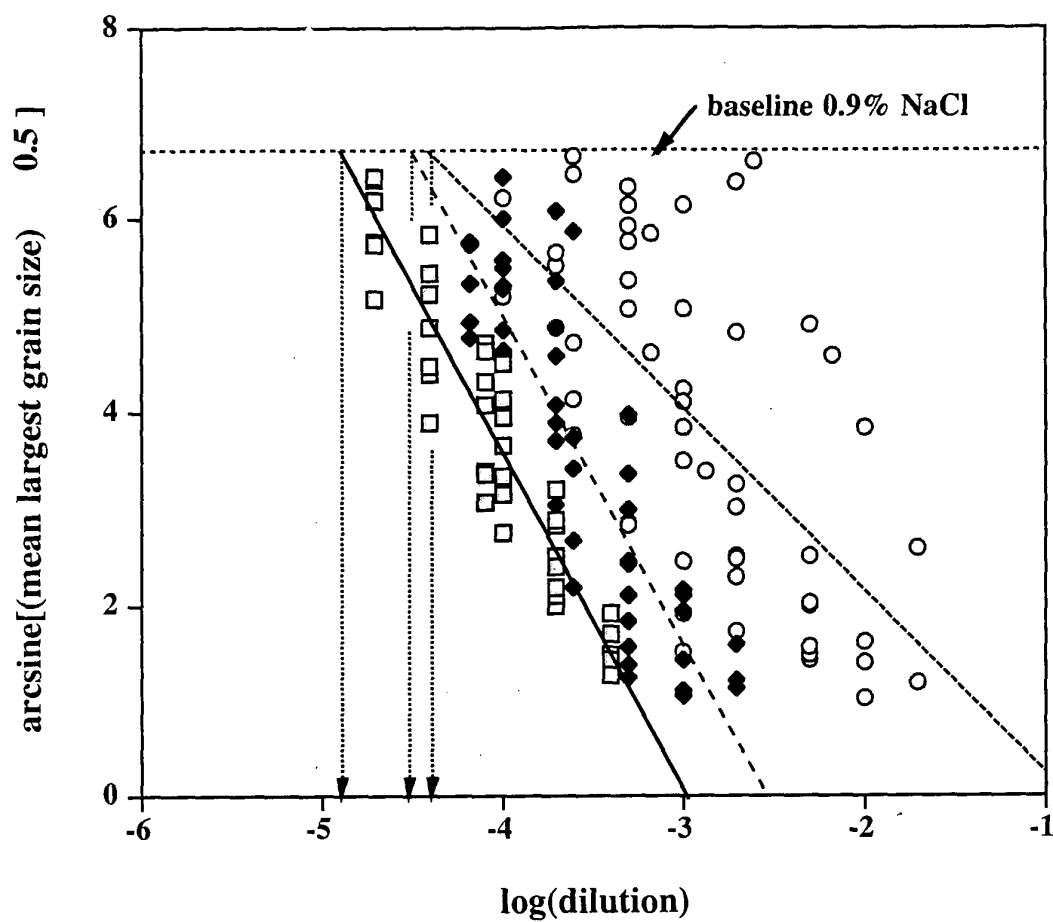


FIG. 8.28

Figure 1 is a graph showing the relationship between the arcsine of the mean largest grain size (in units of 0.5) and the logarithm of dilution. The y-axis is labeled "arcsine[(mean largest grain size) 0.5]" and ranges from 0 to 10. The x-axis is labeled "log(dilution)" and ranges from -5 to -2. Two data series are plotted: open squares and open diamonds. Both series show a linear decrease in grain size as dilution increases. A solid line represents the baseline data (0.9% NaCl at -2°C), and a dashed line represents the data with 0.05% NaCl at -2°C. Vertical dotted lines with arrows indicate the dilution levels for the two data series.

FIG. 8.29

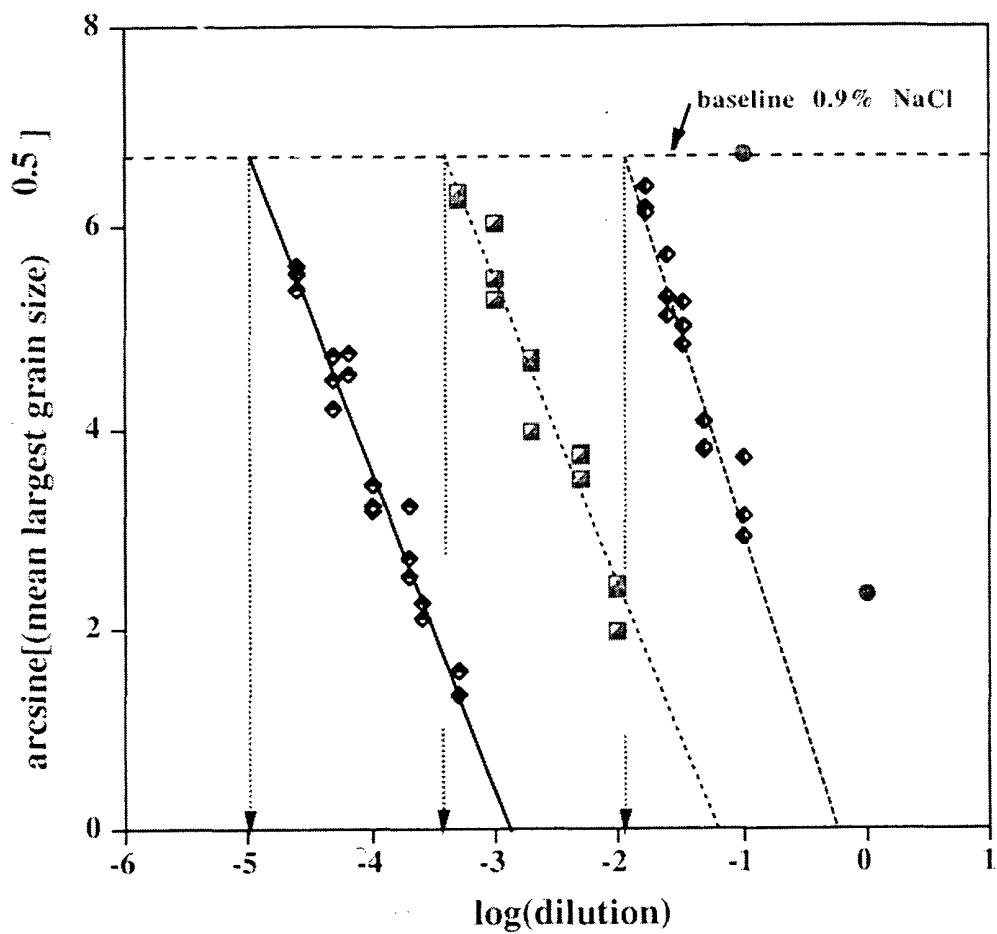


FIG. 8.30

FOI 090-84E92860

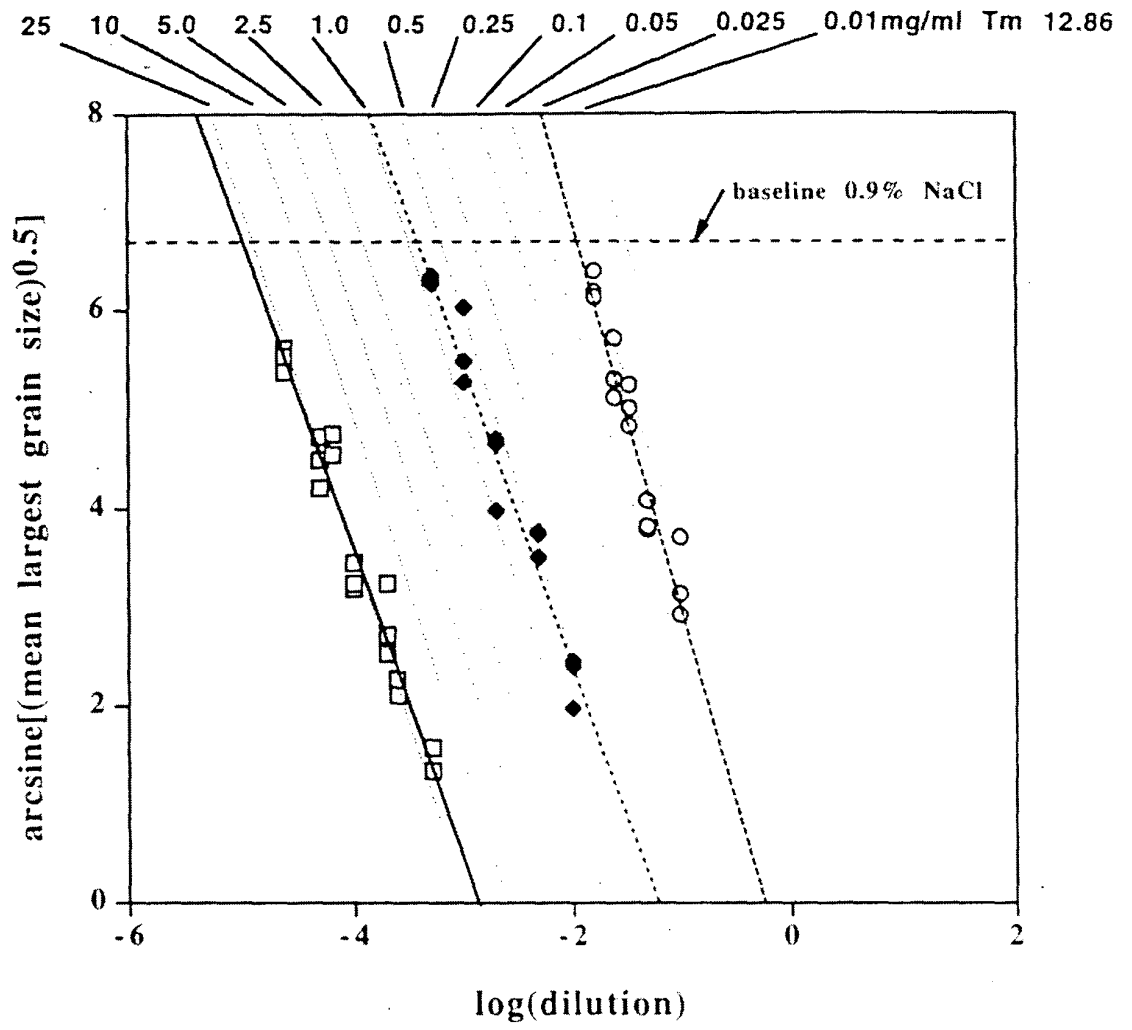


FIG. 8.31

102090" 84E94B60

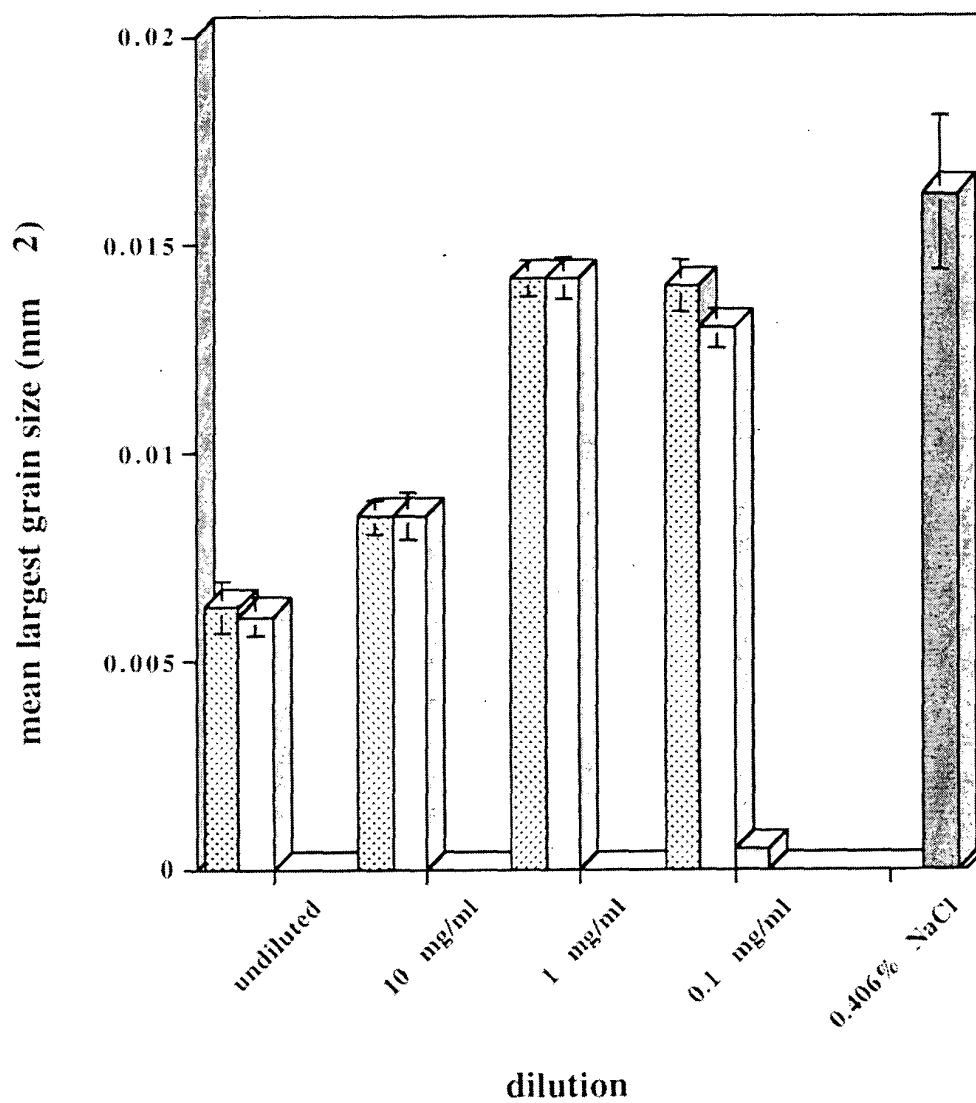


FIG. 8.32

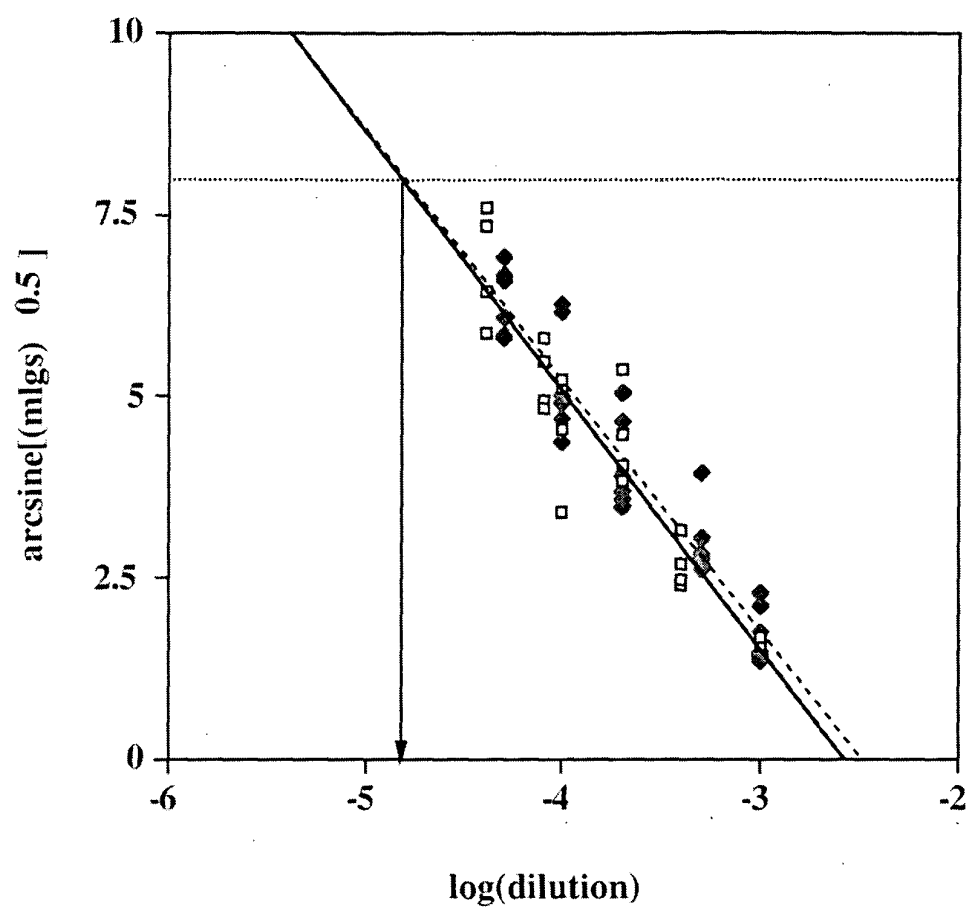


FIG. 8.33

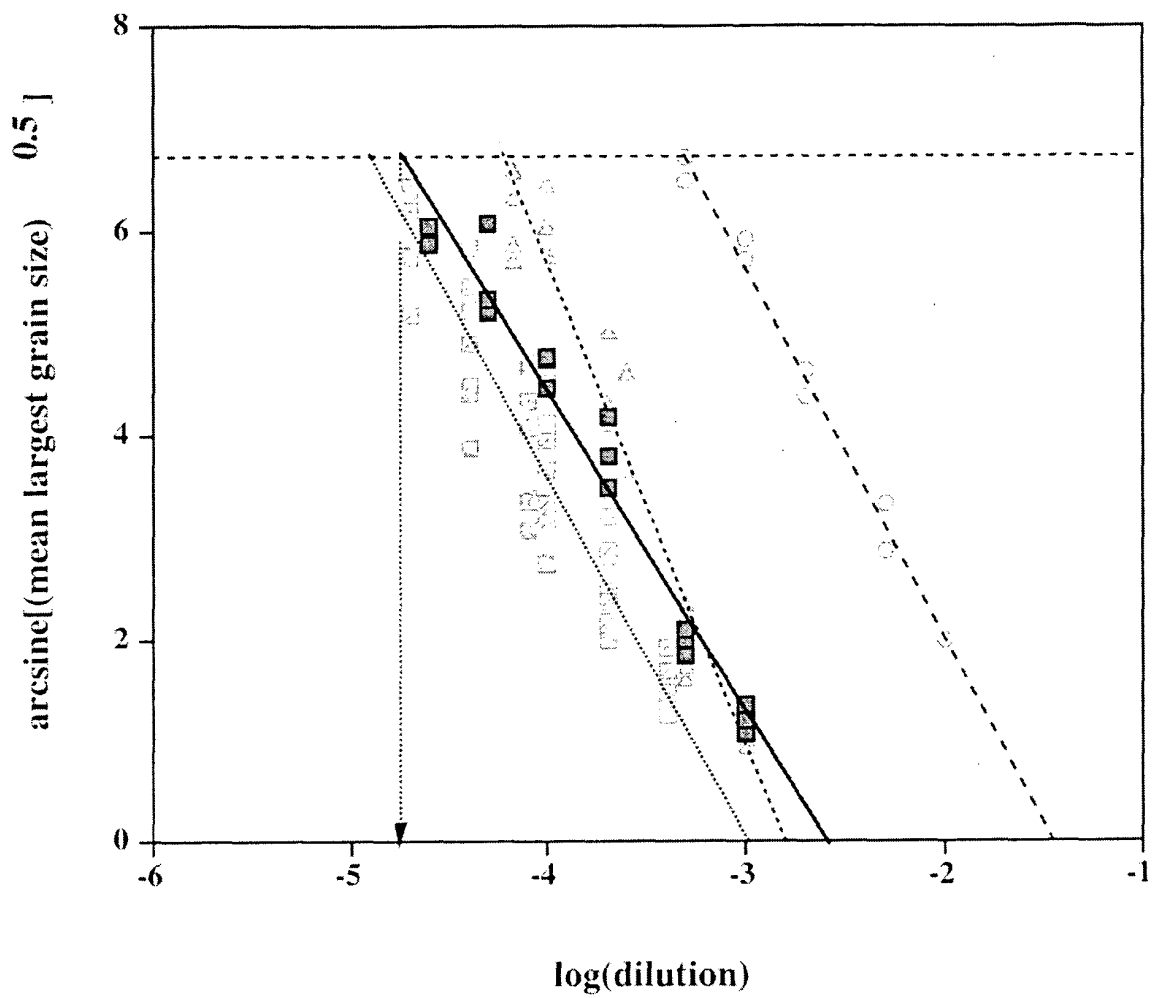


FIG. 8.34

09876348-060701

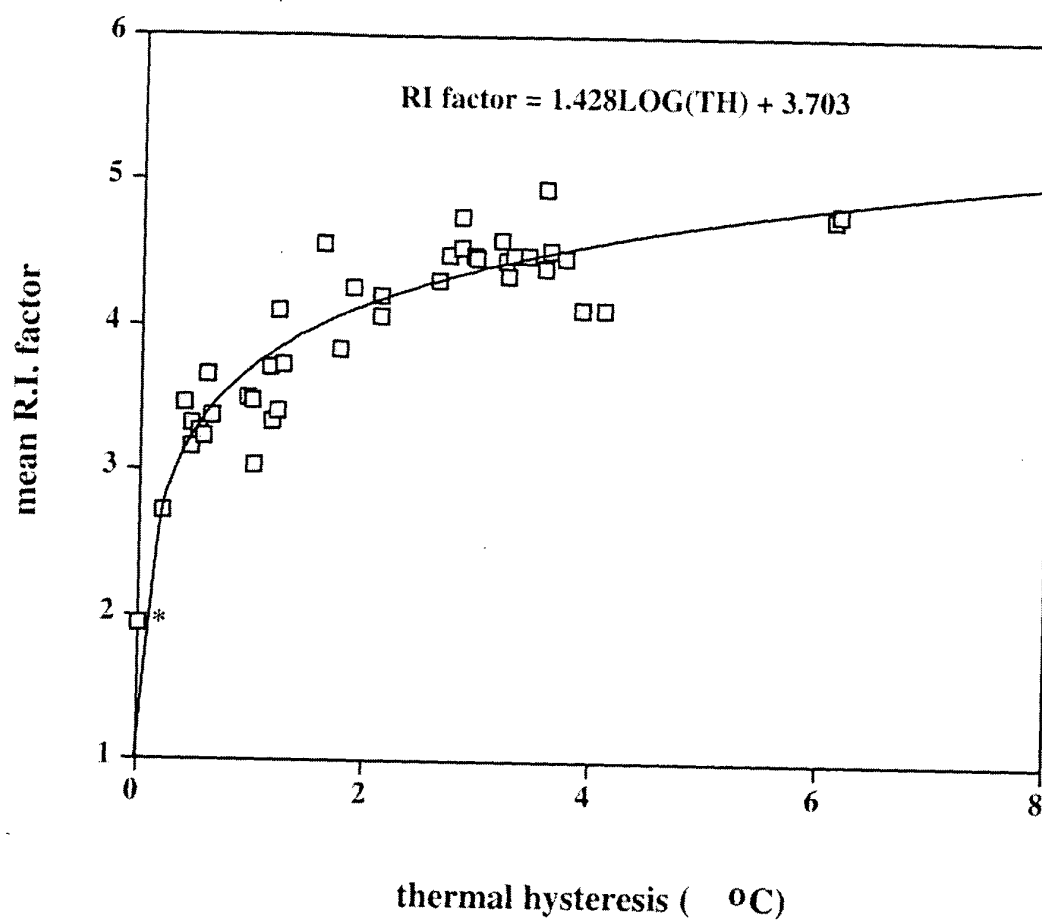


FIG. 8.35

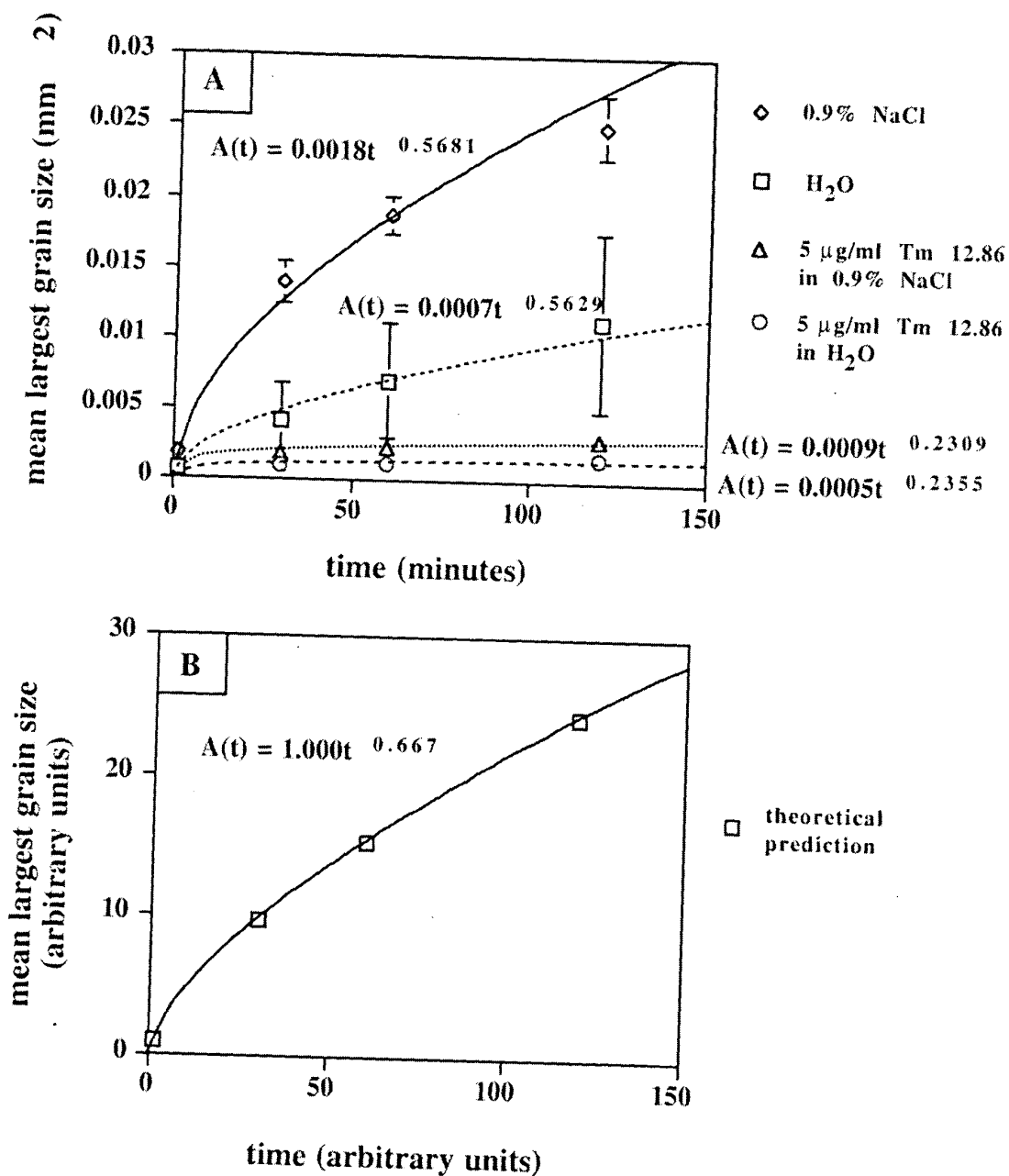


FIG. 8.36

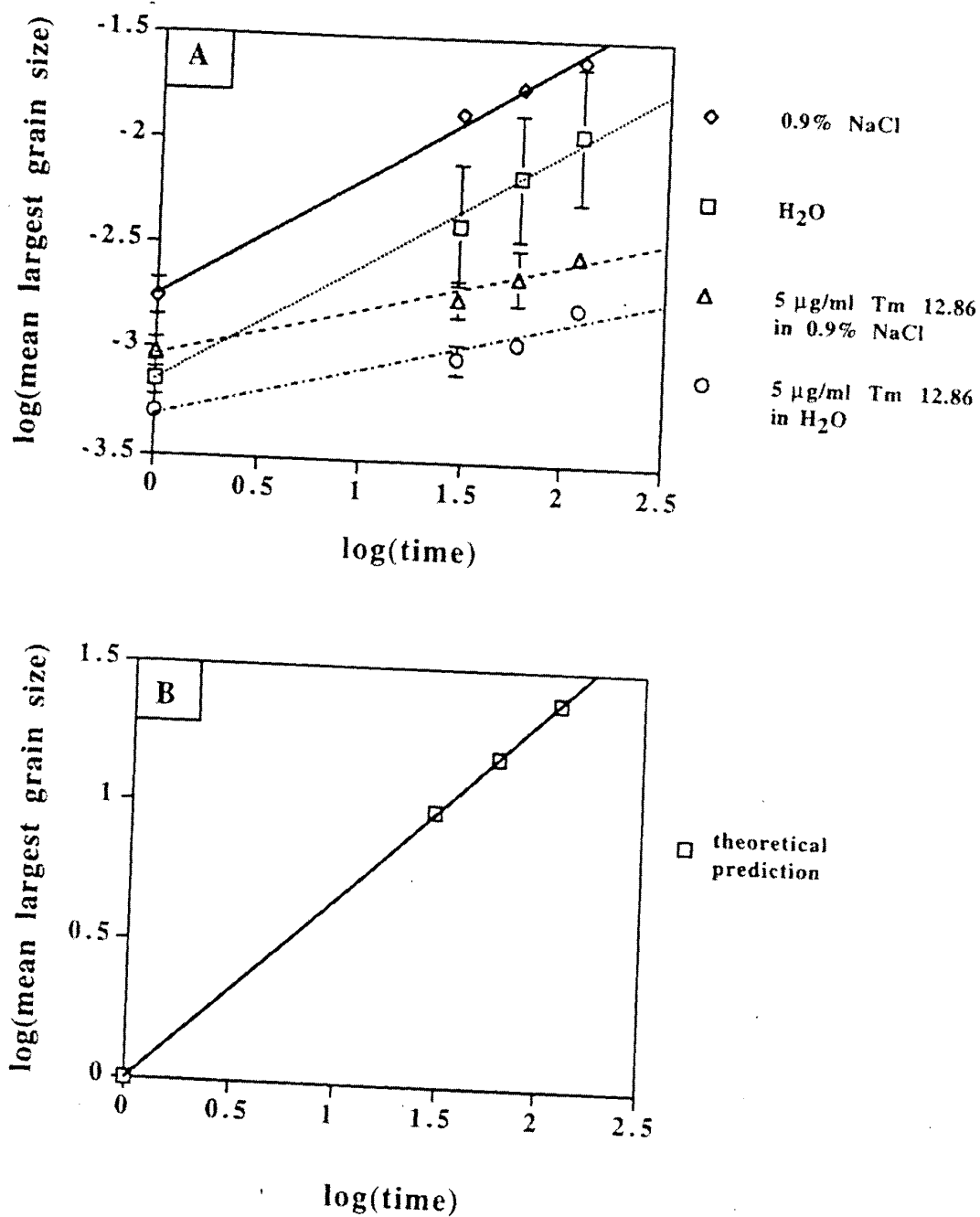
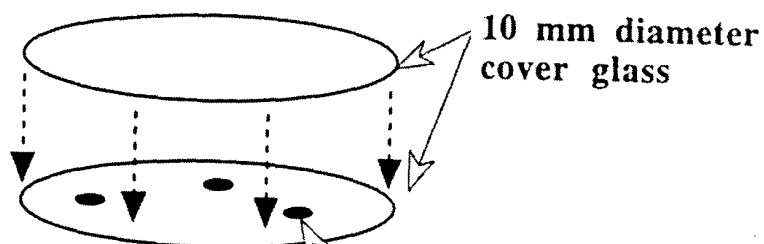


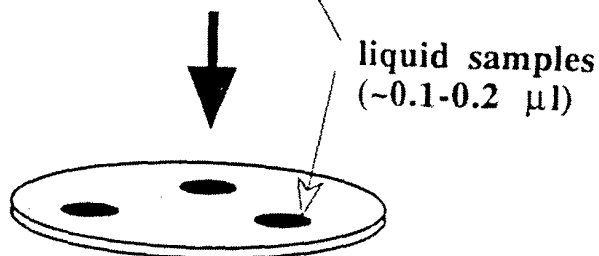
FIG. 8.37

"Sandwich" method of R.I. assessment

1.



2.



3. FREEZE ON ~ -80 C
ALUMINUM PLATE (~ 10 MIN.)



4. PLACE ON COLD STAGE,
ANNEAL AT -6 C UP TO
12+ HOURS

FIG. 8.38

09876348.060701

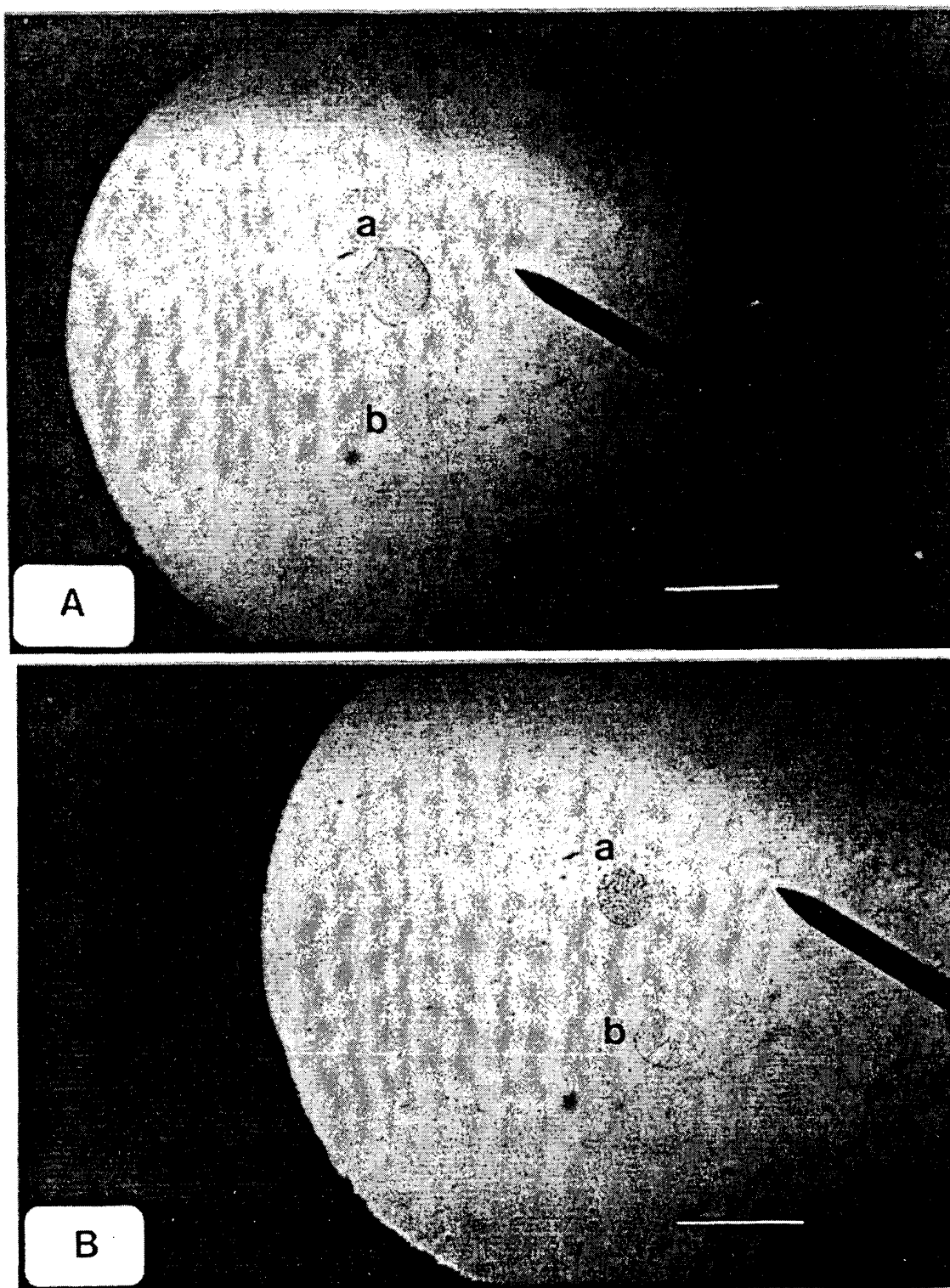


FIG. 8.39

09876348-050704

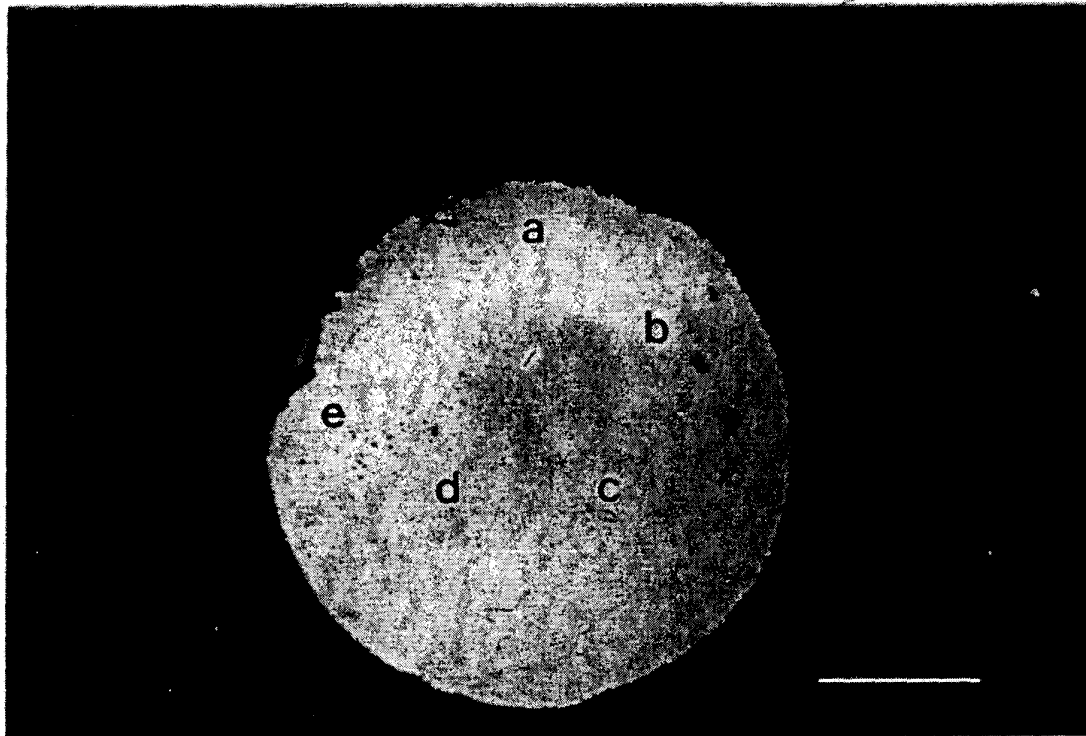


FIG. 8.40

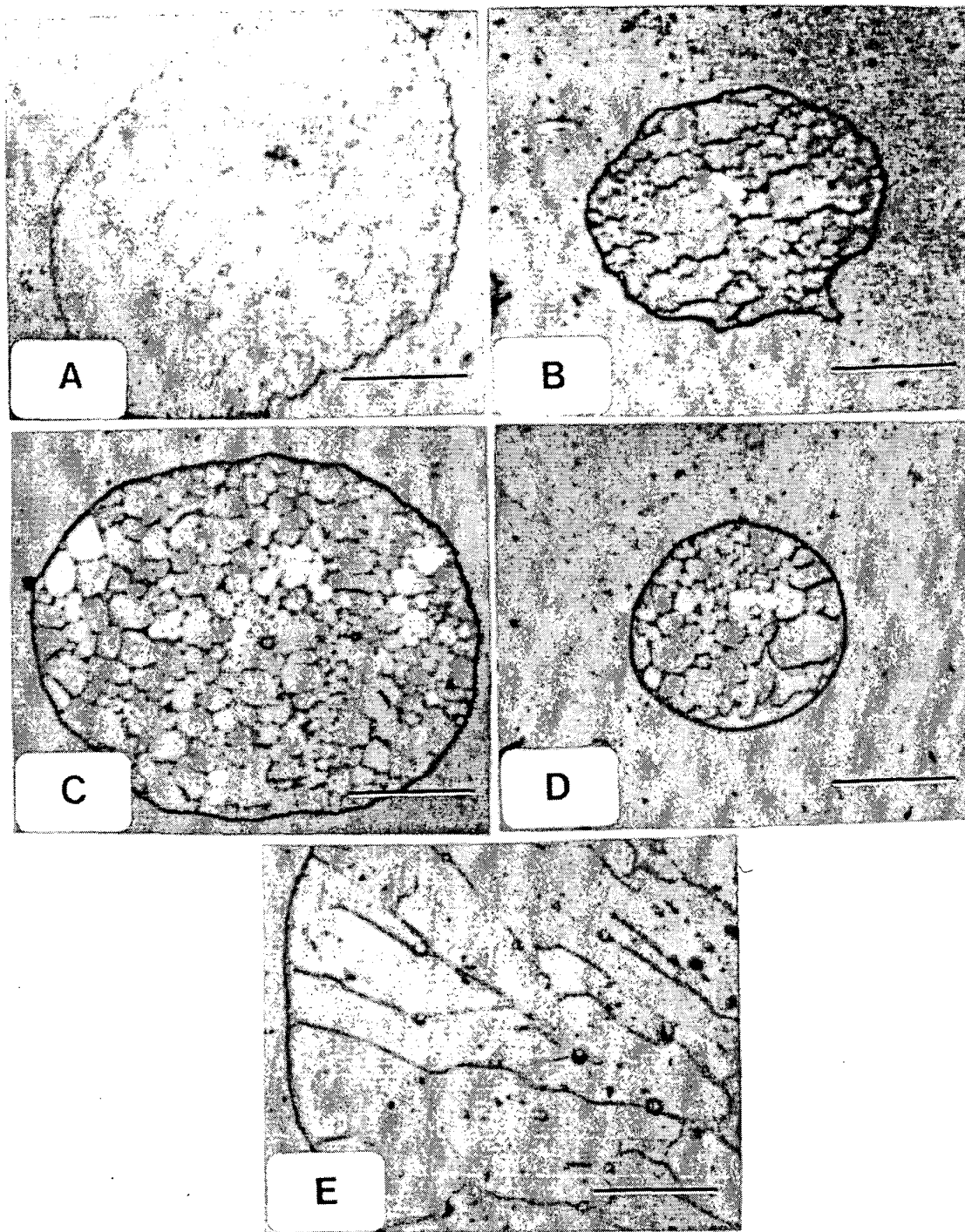


FIG. 8.41

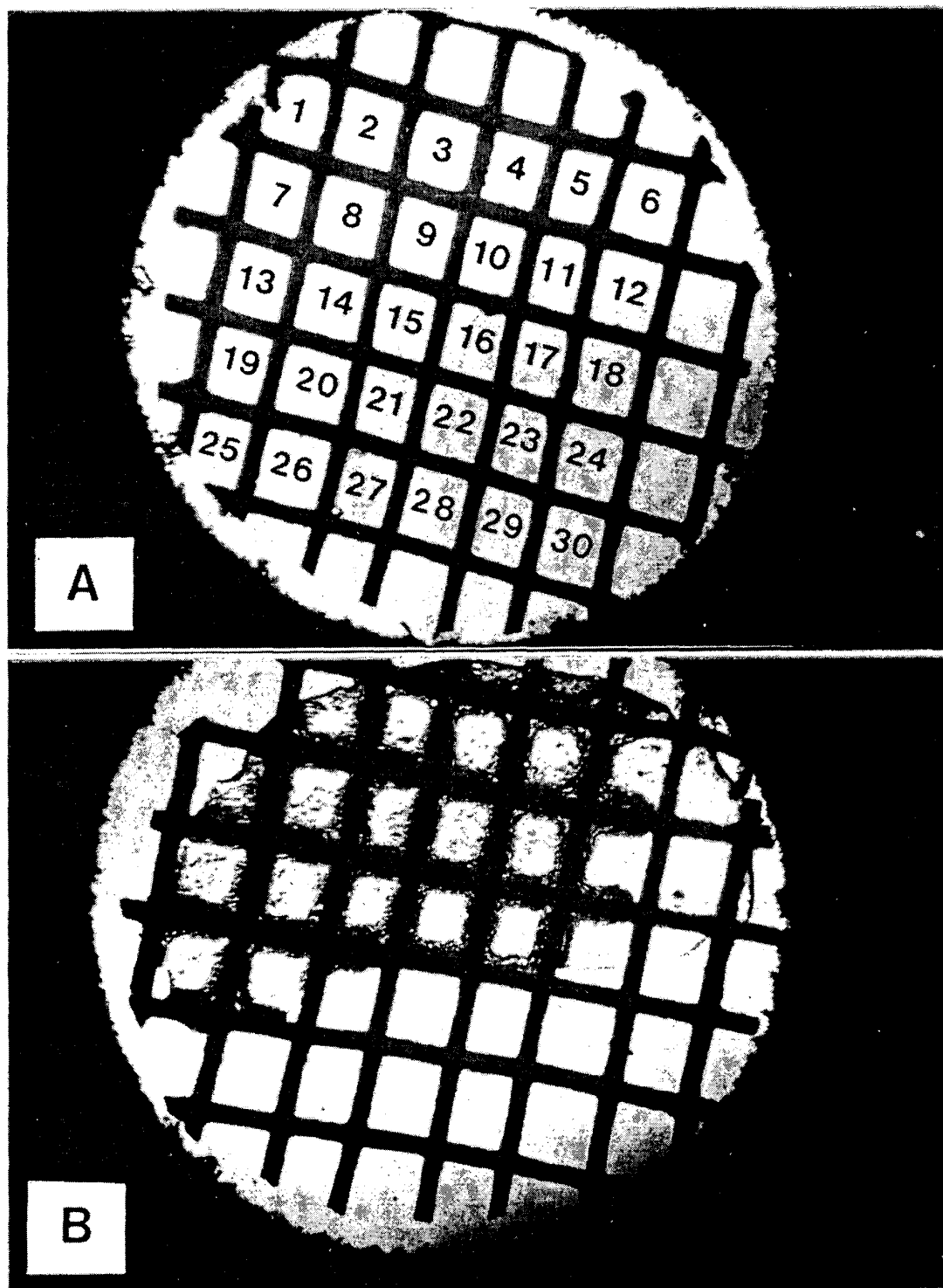


FIG. 8.42

DNA sequence of Tm 13.17 cDNA clone

B	E
a	C
m	O
H	R
I	I

1 AGTGGATCCAAAGAATTTCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTCGCTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACCTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAAATAAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTC
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTTCCACCC

FIG. 8.43

09876348-060701

102090-84548-060701

```

1  GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
      M  K  L  L  L  C  F  A  F  A  A

47  ATCGTCATOGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
      I  V  I  G  A  Q  A  L  T  D  E  Q  I  Q  K

92  AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
      R  N  K  I  S  K  E  C  Q  Q  V  S  G  V  S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
      Q  E  T  I  D  K  V  R  T  G  V  L  V  D  D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
      P  K  M  K  K  H  V  L  C  F  S  K  K  T  G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
      V  A  T  E  A  G  D  T  N  V  E  V  L  K  A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
      K  L  K  H  V  A  S  D  E  E  V  D  K  I  V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
      Q  K  C  V  V  K  K  A  T  P  E  E  T  A  Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCCT
      D  T  F  K  C  I  Y  D  S  K  P  D  F  S  P

406 ATGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
      I  D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

```

polyadenylation signal

poly (A) tail

FIG. 8.44